AM2

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 10:54:58 ; Search time 68 Seconds
(without alignments)
148.828 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 33
Sequence: 1 gcattctagtcgacaagagtttgtcagtgggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19	57.6	2599	6	5266464-1	Patent No. 5266464
	2	18.4	55.8	445	4	US-08-905-223-122	Sequence 122, App
	3	18.4	55.8	460	4	US-08-905-223-120	Sequence 120, App
c	4	18.4	55.8	2102	4	US-09-318-448-19	Sequence 19, Appl
	5	18.4	55.8	2484	4	US-09-293-322C-4	Sequence 4, Appli
c	6	18.2	55.2	12847	1	US-08-550-715-1	Sequence 1, Appli
c	7	18	54.5	4169	4	US-09-166-350-32	Sequence 32, Appl
	8	17.6	53.3	37	1	US-08-388-672A-5	Sequence 5, Appli
	9	17.6	53.3	37	3	US-09-080-554-5	Sequence 5, Appli
c	10	17.6	53.3	150	4	US-08-943-731-85	Sequence 85, Appl
c	11	17.6	53.3	38682	4	US-08-943-731-2	Sequence 2, Appli
c	12	17.6	53.3	152331	3	US-09-128-155-16	Sequence 16, Appl
	13	17.6	53.3	176373	3	US-09-128-155-17	Sequence 17, Appl
	14	17.4	52.7	5261	1	US-08-045-806-3	Sequence 3, Appli
	15	17.4	52.7	5261	1	US-08-366-051B-3	Sequence 3, Appli
c	16	17.4	52.7	72928	3	US-09-009-913-1	Sequence 1, Appli
c	17	17.2	52.1	2844	4	US-09-221-017B-415	Sequence 415, App
	18	17	51.5	1614	4	US-09-134-078-9	Sequence 9, Appli
	19	16.8	50.9	2429	4	US-09-360-545-68	Sequence 68, Appl
c	20	16.8	50.9	8855	2	US-08-542-003-1	Sequence 1, Appli
c	21	16.8	50.9	8855	2	US-08-322-760A-1	Sequence 1, Appli
c	22	16.8	50.9	8855	4	US-09-236-949-1	Sequence 1, Appli
	23	16.6	50.3	230	3	US-08-974-180-10	Sequence 10, Appl
	24	16.6	50.3	345	3	US-08-974-180-9	Sequence 9, Appli
c	25	16.6	50.3	640	4	US-09-221-017B-42	Sequence 42, Appl
c	26	16.6	50.3	2026	4	US-09-324-455-1	Sequence 1, Appli
	27	16.6	50.3	2970	3	US-08-974-180-14	Sequence 14, Appl
	28	16.6	50.3	3311	2	US-08-239-276-10	Sequence 10, Appl
	29	16.6	50.3	3311	2	US-08-468-579B-10	Sequence 10, Appl
	30	16.6	50.3	3311	3	US-08-468-577B-10	Sequence 10, Appl
	31	16.6	50.3	3613	4	US-08-514-213A-1	Sequence 1, Appli
	32	16.6	50.3	6476	4	US-09-127-670-5	Sequence 5, Appli
	33	16.6	50.3	21234	4	US-09-810-671-3	Sequence 3, Appli
c	34	16.6	50.3	36741	4	US-09-301-665-3	Sequence 3, Appli
c	35	16.6	50.3	81001	4	US-09-750-580-1	Sequence 1, Appli
	36	16.4	49.7	3600	5	PCT-US95-13749-1	Sequence 1, Appli
	37	16.4	49.7	12047	2	US-09-022-461-1	Sequence 1, Appli
	38	16.4	49.7	12047	4	US-09-033-556-3	Sequence 3, Appli
c	39	16.4	49.7	35100	2	US-08-770-379-19	Sequence 19, Appl
c	40	16.4	49.7	35100	4	US-08-757-669A-19	Sequence 19, Appl
c	41	16.4	49.7	35100	4	US-09-230-371A-19	Sequence 19, Appl
c	42	16.2	49.1	38	4	US-08-811-481-19	Sequence 19, Appl
	43	16.2	49.1	682	1	US-08-463-115-21	Sequence 21, Appl
	44	16.2	49.1	682	1	US-08-465-388-21	Sequence 21, Appl
c	45	16.2	49.1	1620	6	5449756-10	Patent No. 5449756

ALIGNMENTS

RESULT 1
5266464-1/c
;Patent No. 5266464
; APPLICANT: HOUSEY, GERARD
; TITLE OF INVENTION: METHOD OF SCREENING FOR PROTEIN INHIBITORS
;AND ACTIVATORS
; NUMBER OF SEQUENCES: 3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,073
; FILING DATE: 10-AUG-16989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 154,206
; FILING DATE: 10-FEB-1988
;SEQ ID NO:1:
; LENGTH: 2599
5266464-1

Query Match 57.6%; Score 19; DB 6; Length 2599;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AAGAGTTTGTCAGTGGGAG 33
||||||||||||||||||||
Db 2034 AAGAGTTTGTCAGTGGGAG 2016

RESULT 2
US-08-905-223-122
; Sequence 122, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223

```
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  122:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  445 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      TISSUE TYPE:  Brain
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  236..418
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 4.6
;      OTHER INFORMATION:  seq LLLLHGGGHSALS/WA
US-08-905-223-122

  Query Match             55.8%;  Score 18.4;  DB 4;  Length 445;
  Best Local Similarity   78.6%;  Pred. No. 9.1;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTGGG 31
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Db     345 TTCGAGTCTACAAGAGTGGTTCAGAGGG 372


RESULT 3
US-08-905-223-120
; Sequence 120, Application US/08905223
; Patent No. 6222029
;  GENERAL INFORMATION:
;    APPLICANT:  Edwards, Jean-Baptiste D.
;    APPLICANT:  Duelert, Aymeric
;    APPLICANT:  Lacroix, Bruno
;    TITLE OF INVENTION:  5' ESTs FOR SECRETED PROTEINS
;    NUMBER OF SEQUENCES:  503
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Knobbe, Martens, Olson & Bear
;      STREET:  501 West Broadway
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92101-3505
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Win95
;      SOFTWARE:  Word
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/905,223
;      FILING DATE:
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Israelsen, Ned A.
;      REGISTRATION NUMBER:  29,655
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 235-8550
;      TELEFAX:  (619) 235-0176
;  INFORMATION FOR SEQ ID NO:  120:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  460 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  DOUBLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  CDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo Sapiens
;      TISSUE TYPE:  Brain
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  254..436
;      IDENTIFICATION METHOD:  Von Heijne matrix
;      OTHER INFORMATION:  score 4.6
;      OTHER INFORMATION:  seq LLLLHGGGHSALS/WA
US-08-905-223-120

  Query Match             55.8%;  Score 18.4;  DB 4;  Length 460;
  Best Local Similarity   78.6%;  Pred. No. 9.2;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTGGG 31
            ||| |||| |||||||||   |||| |||
Db     363 TTCGAGTCTACAAGAGTGGTTCAGAGGG 390


RESULT 4
US-09-318-448-19/c
; Sequence 19, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
;  APPLICANT: Johnson, William G.
;  APPLICANT: Stenroos, Edward S.
;  TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
;  TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
;  FILE REFERENCE: 601-1-057
;  CURRENT APPLICATION NUMBER: US/09/318,448
;  CURRENT FILING DATE: 1999-05-25
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
;   LENGTH: 2102
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-318-448-19

  Query Match             55.8%;  Score 18.4;  DB 4;  Length 2102;
  Best Local Similarity   78.6%;  Pred. No. 13;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       5 TCTAGTCGACAAGAGTTTGTCAGTGGGA 32
            || ||  | |||||||  ||||||||||
Db    1606 TCCAGCAGGCAAGAGTAGGTCAGTGGGA 1579


RESULT 5
US-09-293-322C-4
; Sequence 4, Application US/09293322C
; Patent No. 6232110
; GENERAL INFORMATION:
;  APPLICANT:  Pallas, David C
;  APPLICANT:  Du, Xianxing
;  TITLE OF INVENTION:  Coding Sequence for Protein Phosphatase Methylesterase,
; Patent No. 6232110
;  TITLE OF INVENTION:  Recombinant DNA Molecules and Methods
;  FILE REFERENCE:  105-97
;  CURRENT APPLICATION NUMBER: US/09/293,322C
;  CURRENT FILING DATE:  1999-04-16
;  PRIOR APPLICATION NUMBER:  US 60/082,202
;  PRIOR FILING DATE:  1998-04-17
;  NUMBER OF SEQ ID NOS:  17
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2484
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (100)..(1257)
US-09-293-322C-4

  Query Match             55.8%;  Score 18.4;  DB 4;  Length 2484;
  Best Local Similarity   78.6%;  Pred. No. 13;
  Matches   22;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      4 TTCTAGTCGACAAGAGTTTGTCAGTGGG 31
          ||| |||| ||||||||   |||| |||
Db    299 TTCGAGTCTACAAGAGTGGTTCAGAGGG 326


RESULT 6
US-08-550-715-1/c
; Sequence 1, Application US/08550715
; Patent No. 5750345
;  GENERAL INFORMATION:
;    APPLICANT:  Bowie, Lemuel J.
;    TITLE OF INVENTION:  Human '-Thalassemia Mutations as a Predictor of
;    TITLE OF INVENTION:  Blood-Related Disorders
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/550,715
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Gass, David A.
;      REGISTRATION NUMBER:  38,153
;      REFERENCE/DOCKET NUMBER:  28493/32834
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312/474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12847 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(6703..6797, 6915..7119, 7262..7387)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(10514..10608, 10726..10930, 11080..11205)
US-08-550-715-1

  Query Match             55.2%;  Score 18.2;  DB 1;  Length 12847;
  Best Local Similarity   74.2%;  Pred. No. 24;
  Matches   23;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGG 31
          |||||| ||  ||| || ||| ||| | |||
Db   9463 GCATTCAAGGGGACCAGGGTTAGTCTGAGGG 9433


RESULT 7
US-09-166-350-32/c
; Sequence 32, Application US/09166350A
; Patent No. 6440663
; GENERAL INFORMATION:
;  APPLICANT: Scanlan, Matthew
;  APPLICANT: Chen, Yao
;  APPLICANT: Stockert, Elisabeth
;  APPLICANT: Old, Lloyd
;  APPLICANT: Jager, Elke
;  APPLICANT: Knuth, Alex
;  TITLE OF INVENTION: Renal Cancer Associated Antigens and
;  TITLE OF INVENTION: Uses Therefor
;  FILE REFERENCE: L0461/7051
;  CURRENT APPLICATION NUMBER: US/09/166,350A
;  CURRENT FILING DATE: 1998-10-05
;  EARLIER APPLICATION NUMBER: US 09/166,350
;  EARLIER FILING DATE: 1998-10-05
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH: 4169
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-166-350-32

  Query Match             54.5%;  Score 18;  DB 4;  Length 4169;
  Best Local Similarity   80.8%;  Pred. No. 23;
  Matches   21;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      4 TTCTAGTCGACAAGAGTTTGTCAGTG 29
          || ||||  ||| || ||||||||||
Db    940 TTATAGTAAACATGAATTTGTCAGTG 915


RESULT 8
US-08-388-672A-5
; Sequence 5, Application US/08388672A
; Patent No. 5795961
;  GENERAL INFORMATION:
;    APPLICANT:  Wallace, T. Paul
;    APPLICANT:  Harris, William J.
;    APPLICANT:  Carr, Frank J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Welt, Sydney
;    APPLICANT:  Kitamura, Kunio
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis B
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe and Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,672A
;      FILING DATE:  14-FEB-1995
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5795961man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5409
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-688-9200
;      TELEFAX:  212-838-3884
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
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;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-08-388-672A-5

  Query Match             53.3%;  Score 17.6;  DB 1;  Length 37;
  Best Local Similarity   65.4%;  Pred. No. 13;
  Matches   17;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       6 CTAGTCGACAAGAGTTTGTCAGTGGG 31
           |||||||||| ||| |:|:: |: :|
Db       2 CTAGTCGACATGAGGTKGYYTGYTSG 27


RESULT 9
US-09-080-554-5
; Sequence 5, Application US/09080554
; Patent No. 6025481
;  GENERAL INFORMATION:
;    APPLICANT:  Wallace, T. Paul
;    APPLICANT:  Harris, William J.
;    APPLICANT:  Carr, Frank J.
;    APPLICANT:  Old, Lloyd J.
;    APPLICANT:  Welt, Sydney
;    APPLICANT:  Kitamura, Kunio
;    TITLE OF INVENTION:  Recombinant Human Anti-Lewis B
;    TITLE OF INVENTION:  Antibodies
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/080,554
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/388,672
;      FILING DATE:  14-FEB-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Halluin, Albert P.
;      REGISTRATION NUMBER:  25,227
;      REFERENCE/DOCKET NUMBER:  7606-032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-854-3660
;      TELEFAX:  415-854-3694
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  37 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  DNA (genomic)
US-09-080-554-5

  Query Match             53.3%;  Score 17.6;  DB 3;  Length 37;
  Best Local Similarity   65.4%;  Pred. No. 13;
  Matches   17;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       6 CTAGTCGACAAGAGTTTGTCAGTGGG 31
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Db       2 CTAGTCGACATGAGGTKGYYTGYTSG 27


RESULT 10
US-08-943-731-85/c
; Sequence 85, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  85:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  150 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-85

  Query Match             53.3%;  Score 17.6;  DB 4;  Length 150;
  Best Local Similarity   71.9%;  Pred. No. 17;
  Matches   23;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           |||||||||  | |||||      ||||||||
Db      42 CATTCTAGTGCAGAAGAGCACAAGAGTGGGAG 11


RESULT 11
US-08-943-731-2/c
; Sequence 2, Application US/08943731
; Patent No. 6265157
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  PROCKOP, DARWIN J.
;    APPLICANT:  SPOTILA, LORETTA D.
;    APPLICANT:  DELTAS, CONSTANTINOS D.
;    APPLICANT:  SEREDA, LARISA
;    APPLICANT:  LARSON, ANDREA W.
;    APPLICANT:  PACK, MICHAEL
;    APPLICANT:  COLIGE, ALAIN
;    APPLICANT:  EARLY, JAMES
;    APPLICANT:  KORKKO, JARMO
;    APPLICANT:  ALA-KOKKO, LEENA, et al.
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR DETECTING
;    TITLE OF INVENTION:  ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
;    NUMBER OF SEQUENCES:  666
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PANITCH SCHWARZE JACOBS & NADEL, P.C.
;      STREET:  ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
;      STREET:  FLR.
;      CITY:  PHILADELPHIA
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103-7086
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/943,731
;      FILING DATE:  03-OCT-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/212,322
;      FILING DATE:  14-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/803,628
;      FILING DATE:  03-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DOYLE LEARY Ph.D., KATHRYN
;      REGISTRATION NUMBER:  36,317
;      REFERENCE/DOCKET NUMBER:  9598-27
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-965-1284
;      TELEFAX:  215-567-2991
;      TELEX:  831-494
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  38682 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-943-731-2

  Query Match             53.3%;  Score 17.6;  DB 4;  Length 38682;
  Best Local Similarity   71.9%;  Pred. No. 58;
  Matches   23;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           |||||||||  | |||||      ||||||||
Db   21154 CATTCTAGTGCAGAAGAGCACAAGAGTGGGAG 21123


RESULT 12
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match             53.3%;  Score 17.6;  DB 3;  Length 152331;
  Best Local Similarity   71.9%;  Pred. No. 77;
  Matches   23;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           |||  | |   ||||||| ||||||  |||||
Db 115561 GCAAGCCAAGTGACAAGATTTTGTCCCTGGGA 115530


RESULT 13
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 17
;   LENGTH: 176373
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(176373)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

  Query Match             53.3%;  Score 17.6;  DB 3;  Length 176373;
  Best Local Similarity   71.9%;  Pred. No. 79;
  Matches   23;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           |||  | |   ||||||| ||||||  |||||
Db   63844 GCAAGCCAAGTGACAAGATTTTGTCCCTGGGA 63875


RESULT 14
US-08-045-806-3
; Sequence 3, Application US/08045806
; Patent No. 5378822
;  GENERAL INFORMATION:
;    APPLICANT:  Bradfield, Christopher Alan
;    APPLICANT:  Dolwick, Kristin Marie
;    APPLICANT:  Poland, Alan
;    TITLE OF INVENTION:  Ah Receptor cDNA and Method of
;    TITLE OF INVENTION:  Determining Human Risks To Environmental Pollutants
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Tilton, Fallon, Lungmus & Chestnut
;       STREET:  100 South Wacker Drive, Suite 960
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606-4002
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/045,806
;       FILING DATE:  19930408
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Fentress, Susan B.
;       REGISTRATION NUMBER:  31,327
;       REFERENCE/DOCKET NUMBER:  NU-9207
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312)-456-8000
;       TELEFAX:  (312)-456-7776
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5261 base pairs
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  383..2927
US-08-045-806-3

  Query Match             52.7%;  Score 17.4;  DB 1;  Length 5261;
  Best Local Similarity   77.8%;  Pred. No. 47;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTGG 30
           |||||||  | ||||  |||||||  | |
Db    2578 TTCTAGTTTAGAAGATTTTGTCACTTG 2604


RESULT 15
US-08-366-051B-3
; Sequence 3, Application US/08366051B
; Patent No. 5650283
;  GENERAL INFORMATION:
;     APPLICANT:  Bradfield, Christopher A.
;     APPLICANT:  Dolwick, Kristin M.
;     APPLICANT:  Carver, Lucy A.
;     TITLE OF INVENTION:  Ah Receptor cDNAs and Genetically
;     TITLE OF INVENTION:  Engineered Cells for Detecting Agonists to the Ah
;     TITLE OF INVENTION:  Receptor
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Tilton, Fallon, Lungmus & Chestnut
;       STREET:  100 South Wacker Drive, Suite 960
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606-4002
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/366,051B
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Tilton, Timothy L.
;       REGISTRATION NUMBER:  16,926
;       REFERENCE/DOCKET NUMBER:  NU-9207-CIP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312)-456-8000
;       TELEFAX:  (312)-456-7776
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5261 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  383..2927
US-08-366-051B-3

  Query Match             52.7%;  Score 17.4;  DB 1;  Length 5261;
  Best Local Similarity   77.8%;  Pred. No. 47;
  Matches   21;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTGG 30
           |||||||  | ||||  |||||||  | |
Db    2578 TTCTAGTTTAGAAGATTTTGTCACTTG 2604


Search completed: December 16, 2002, 10:57:22
Job time : 128 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 10:54:59 ; Search time 2429 Seconds
(without alignments)
220.029 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 33
Sequence: 1 gcattctagtcgacaagagtttgtcagtgggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	21.4	64.8	1061	17	BH677152	BH677152 BOMKA35TR
	2	21.2	64.2	788	12	BG780076	BG780076 SEAUMC000
c	3	20.8	63.0	427	17	BH252660	BH252660 SALK_0137
	4	20.8	63.0	1029	10	BE563270	BE563270 601335580
c	5	20.6	62.4	698	17	AZ613804	AZ613804 1M0442017
	6	20.4	61.8	660	17	AG116222	AG116222 Pan trogl
	7	20.4	61.8	766	12	BG614194	BG614194 602641866
	8	20.2	61.2	252	9	AA359569	AA359569 EST68605
c	9	20	60.6	403	14	D26831	D26831 CELK009EZF
c	10	20	60.6	466	12	BF851402	BF851402 IL5-EN008
	11	20	60.6	697	13	BI224033	BI224033 602942940
	12	20	60.6	728	17	BH598122	BH598122 BOGLZ53TF
	13	20	60.6	833	17	BH449843	BH449843 BOGRE19TR
c	14	20	60.6	978	13	BM468802	BM468802 AGENCOURT
c	15	19.8	60.0	240	10	BB150049	BB150049 BB150049
c	16	19.8	60.0	281	10	BB159127	BB159127 BB159127
c	17	19.8	60.0	444	12	BF490151	BF490151 AT26449.5
	18	19.8	60.0	611	17	AZ832714	AZ832714 2M0113K10
	19	19.8	60.0	886	12	BF030538	BF030538 601559867
c	20	19.8	60.0	940	17	AG077093	AG077093 Pan trogl
	21	19.6	59.4	219	12	BE827967	BE827967 RC4-ET002
c	22	19.6	59.4	401	13	BM448487	BM448487 DSA011F07
c	23	19.6	59.4	407	12	BF996133	BF996133 RC3-GN004
	24	19.6	59.4	586	9	AU199787	AU199787 AU199787
	25	19.6	59.4	615	13	BJ120449	BJ120449 BJ120449
c	26	19.6	59.4	770	13	BI824720	BI824720 603033888
c	27	19.4	58.8	183	10	AV785600	AV785600 AV785600
	28	19.4	58.8	267	10	BB576883	BB576883 BB576883
	29	19.4	58.8	413	10	BE068204	BE068204 CM1-BT036
	30	19.4	58.8	556	17	AQ113920	AQ113920 CIT-HSP-2
c	31	19.4	58.8	620	17	AZ804633	AZ804633 2M0065M10
c	32	19.2	58.2	235	10	AW761254	AW761254 sl65c01.y
c	33	19.2	58.2	329	9	AA874978	AA874978 UI-R-E0-c
c	34	19.2	58.2	340	9	AI452286	AI452286 mp90c02.x
	35	19.2	58.2	345	9	AU110888	AU110888 AU110888
c	36	19.2	58.2	386	9	AA719026	AA719026 ah46c01.s
c	37	19.2	58.2	390	12	BF440482	BF440482 BS2900014
c	38	19.2	58.2	424	17	AQ845191	AQ845191 am44e08 J
c	39	19.2	58.2	425	9	AA451381	AA451381 vf81a03.r
c	40	19.2	58.2	461	9	AI045963	AI045963 UI-R-C1-j
	41	19.2	58.2	489	13	BJ481882	BJ481882 BJ481882
c	42	19.2	58.2	507	13	BJ292333	BJ292333 BJ292333
	43	19.2	58.2	514	12	BF630170	BF630170 HVSMEb000
c	44	19.2	58.2	529	9	AA690593	AA690593 vu53d05.r
	45	19.2	58.2	540	9	AJ470270	AJ470270 AJ470270

ALIGNMENTS

RESULT 1
BH677152/c
LOCUS BH677152 1061 bp DNA linear GSS 19-FEB-2002
DEFINITION BOMKA35TR BO_2_3_KB Brassica oleracea genomic clone BOMKA35, DNA sequence.
ACCESSION BH677152
VERSION BH677152.1 GI:18747595
KEYWORDS GSS.
SOURCE Brassica oleracea.
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 1061)
AUTHORS Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
TITLE Whole genome shotgun sequencing of Brassica oleracea
JOURNAL Unpublished (2001)
COMMENT Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
FEATURES Location/Qualifiers
source 1. .1061
/organism="Brassica oleracea"

```
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMKA35"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      267 a    267 c    242 g    285 t
ORIGIN

  Query Match             64.8%;  Score 21.4;  DB 17;  Length 1061;
  Best Local Similarity   80.6%;  Pred. No. 97;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           ||| || ||  |||||||||||||| | ||||
Db     342 ATTTTATTCATCAAGAGTTTGTCACTAGGAG 312


RESULT 2
BG780076
LOCUS       BG780076                 788 bp    mRNA    linear   EST 20-MAY-2001
DEFINITION  SEAUMC000033 Sea urchin primary mesenchyme cell cDNA library
            Strongylocentrotus purpuratus cDNA clone 91214953_PC_0022_B2_C09_MR
            5', mRNA sequence.
ACCESSION   BG780076
VERSION     BG780076.1  GI:14151089
KEYWORDS    EST.
SOURCE      Strongylocentrotus purpuratus.
  ORGANISM  Strongylocentrotus purpuratus
            Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
            Echinoidea; Euechinoidea; Echinacea; Echinoida;
            Strongylocentrotidae; Strongylocentrotus.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   Zhu,X., Mahairas,G., Illies,M.R., Cameron,R.A., Davidson,E.H. and
            Ettensohn,C.A.
  TITLE     A large scale analysis of mRNAs expressed by primary mesenchyme
            cells of the sea urchin embryo
  JOURNAL   Development 128 (13), 2615-2627 (2001)
  MEDLINE   21384984
COMMENT     Contact: Ettensohn CA
            Dept. Biol. Sci.
            Carnegie Mellon University
            4400 Fifth Avenue, Pittsburgh, PA 15213, USA
            Tel: +1 412 268 5849
            Email: ettensohn@andrew.cmu.edu.
FEATURES             Location/Qualifiers
     source          1. .788
                     /organism="Strongylocentrotus purpuratus"
                     /db_xref="taxon:7668"
                     /clone="91214953_PC_0022_B2_C09_MR"
                     /clone_lib="Sea urchin primary mesenchyme cell cDNA
                     library"
                     /tissue_type="embryo"
                     /cell_type="primary mesenchyme cells"
                     /lab_host="E.coli"
                     /note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; oligo
                     dt priming from poly A+ RNA, directionally cloned"
BASE COUNT      210 a    143 c    159 g    276 t
ORIGIN

  Query Match             64.2%;  Score 21.2;  DB 12;  Length 788;
  Best Local Similarity   88.5%;  Pred. No. 1e+02;
  Matches   23;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTG 29
           |||| ||||||| |||||||||||| |
Db     727 TTCTTGTCGACATGAGTTTGTCAGCG 752


RESULT 3
BH252660/c
LOCUS       BH252660                 427 bp    DNA     linear   GSS 28-NOV-2001
DEFINITION  SALK_013711 Arabidopsis thaliana TDNA insertion lines Arabidopsis
            thaliana genomic clone SALK_013711, DNA sequence.
ACCESSION   BH252660
VERSION     BH252660.1  GI:17139638
KEYWORDS    GSS.
SOURCE      thale cress.
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1  (bases 1 to 427)
  AUTHORS   Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab
            ,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P.
            , Zimmerman,J. and Ecker,J.R.
  TITLE     A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA.
            Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source          1. .427
                     /organism="Arabidopsis thaliana"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_013711"
                     /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains  one or more TDNA insertion
                     elements. The resultant fragment for each  line was
                     directly sequenced to determine the genomic sequence at
                     the  site of insertion. Details of the protocols used can
                     be found at  http://signal.salk.edu/tdna_protocols.html"
BASE COUNT      110 a    111 c     87 g    111 t      8 others
ORIGIN

  Query Match             63.0%;  Score 20.8;  DB 17;  Length 427;
  Best Local Similarity   78.1%;  Pred. No. 1.1e+02;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           | ||||||||| |||||||   || ||||| |
Db      63 GAATTCTAGTCAACAAGAGGGCGTAAGTGGTA 32


RESULT 4
BE563270
LOCUS       BE563270                1029 bp    mRNA    linear   EST 15-AUG-2000
DEFINITION  601335580F1 NIH_MGC_39 Homo sapiens cDNA clone IMAGE:3689707 5',
            mRNA sequence.
ACCESSION   BE563270
VERSION     BE563270.1  GI:9807082
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1029)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
```

```
           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM384  row: o  column: 20
           High quality sequence stop: 669.
FEATURES             Location/Qualifiers
     source          1. .1029
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3689707"
                     /clone_lib="NIH_MGC_39"
                     /tissue_type="adenocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California,  Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies)."
BASE COUNT      314 a    232 c    302 g    181 t
ORIGIN

  Query Match            63.0%;  Score 20.8;  DB 10;  Length 1029;
  Best Local Similarity  91.7%;  Pred. No. 1.8e+02;
  Matches   22;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      8 AGTCGACAAGAGTTTGTCAGTGGG 31
          | | ||||||||||||||||||||
Db    763 AATTGACAAGAGTTTGTCAGTGGG 786


RESULT 5
AZ613804/c
LOCUS       AZ613804                 698 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0442O17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0442O17 F, DNA sequence.
ACCESSION   AZ613804
VERSION     AZ613804.1  GI:11735994
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 698)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0442  row: O  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 698.
FEATURES             Location/Qualifiers
     source          1. .698
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0442O17"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      198 a    150 c    161 g    189 t
ORIGIN

  Query Match            62.4%;  Score 20.6;  DB 17;  Length 698;
  Best Local Similarity  85.2%;  Pred. No. 1.7e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      3 ATTCTAGTCGACAAGAGTTTGTCAGTG 29
          ||||||| | |||||| |||||||| |
Db    414 ATTCTAGCCAACAAGAATTTGTCAGGG 388


RESULT 6
AG116222
LOCUS       AG116222                 660 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-123L03.R, genomic survey sequence.
ACCESSION   AG116222
VERSION     AG116222.1  GI:16736741
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-123L03.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 660)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-123L03.R"
```

```
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT       187 a    135 c    126 g    212 t
ORIGIN

  Query Match             61.8%;  Score 20.4;  DB 17;  Length 660;
  Best Local Similarity   80.0%;  Pred. No. 2.1e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           ||||| ||| |  | ||||||||||||| |
Db     564 ATTCTTGTCAAGGAAAGTTTGTCAGTGGAA 593


RESULT 7
BG614194
LOCUS       BG614194                 766 bp    mRNA    linear   EST 18-APR-2001
DEFINITION  602641866F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4772705 5',
            mRNA sequence.
ACCESSION   BG614194
VERSION     BG614194.1  GI:13665565
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1643  row: d  column: 18
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
     source          1. .766
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4772705"
                     /clone_lib="NIH_MGC_61"
                     /tissue_type="embryonal carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
BASE COUNT       214 a    169 c    143 g    240 t
ORIGIN

  Query Match             61.8%;  Score 20.4;  DB 12;  Length 766;
  Best Local Similarity   80.0%;  Pred. No. 2.3e+02;
  Matches   24;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           ||||| ||| |  | ||||||||||||| |
Db     279 ATTCTTGTCAAGGAAAGTTTGTCAGTGGAA 308


RESULT 8
AA359569
LOCUS       AA359569                 252 bp    mRNA    linear   EST 21-APR-1997
DEFINITION  EST68605 Fetal lung II Homo sapiens cDNA 5' end, mRNA sequence.
ACCESSION   AA359569
VERSION     AA359569.1  GI:2011885
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 252)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
            ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
            , Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
            Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
            ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
            Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
COMMENT     Other_ESTs: THC77447
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .252
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):163683"
                     /db_xref="taxon:9606"
                     /clone_lib="Fetal lung II"
                     /sex="male"
                     /dev_stage="fetus, 19 wks"
                     /note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
                     ; Site_2: XhoI"
BASE COUNT       45 a     86 c     67 g     51 t      3 others
ORIGIN

  Query Match             61.2%;  Score 20.2;  DB 9;  Length 252;
  Best Local Similarity   75.8%;  Pred. No. 1.5e+02;
  Matches   25;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           || ||||| ||  |||| ||||| |  ||||||
Db     209 GCCTTCTATTCTGCAAGTGTTTGACTTTGGGAG 241


RESULT 9
D26831/c
LOCUS       D26831                   403 bp    mRNA    linear   EST 20-NOV-1995
DEFINITION  CELK009EZF Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA
            clone yk9e12 5', mRNA sequence.
```

```
ACCESSION   D26831
VERSION     D26831.1  GI:521769
KEYWORDS    EST.
SOURCE      Caenorhabditis elegans.
  ORGANISM  Caenorhabditis elegans
            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
            ; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE   1  (bases 1 to 403)
  AUTHORS   Kohara,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
            Tabara,H.
  TITLE     Toward an expression map of the C.elegans genome
  JOURNAL   Unpublished (1994)
COMMENT     Contact: Yuji Kohara
            Genome Biology Lab.
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411, Japan
            Tel: 81-559-81-6854
            Fax: 81-559-81-6855
            Email: ykohara@lab.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .403
                     /organism="Caenorhabditis elegans"
                     /strain="CB1489 him-8(e1489)"
                     /db_xref="taxon:6239"
                     /clone="yk9e12"
                     /clone_lib="Yuji Kohara unpublished cDNA"
                     /sex="hermaphrodite, male"
                     /tissue_type="whole animal"
                     /dev_stage="varied"
BASE COUNT      133 a     78 c     88 g    102 t      2 others
ORIGIN

  Query Match             60.6%;  Score 20;  DB 14;  Length 403;
  Best Local Similarity   82.1%;  Pred. No. 2.4e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGG 30
           ||||| || ||||||  ||||| |||||
Db     168 ATTCTGGTTGACAAGCTTTTGTGAGTGG 141


RESULT 10
BF851402/c
LOCUS       BF851402                466 bp    mRNA    linear   EST 16-JAN-2001
DEFINITION  IL5-EN0086-281100-282-f08 EN0086 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BF851402
VERSION     BF851402.1  GI:12238564
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 466)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=IL5&t2=IL5-EN0086-
            281100-282-f08&t3=2000-11-28&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 396.
FEATURES             Location/Qualifiers
     source          1. .466
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="EN0086"
                     /dev_stage="Adult"
                     /note="Organ: lung_normal; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       98 a    132 c    123 g    112 t      1 others
ORIGIN

  Query Match             60.6%;  Score 20;  DB 12;  Length 466;
  Best Local Similarity   82.1%;  Pred. No. 2.6e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       5 TCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           |||||  | |||||||  ||||||||||
Db     358 TCTAGCAGGCAAGAGTAGGTCAGTGGGA 331


RESULT 11
BI224033
LOCUS       BI224033                697 bp    mRNA    linear   EST 11-JUL-2001
DEFINITION  602942940F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5106272 5',
            mRNA sequence.
ACCESSION   BI224033
VERSION     BI224033.1  GI:14677477
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 697)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: Incyte Genomics, Inc.
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11256  row: o  column: 09
            High quality sequence stop: 614.
FEATURES             Location/Qualifiers
     source          1. .697
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5106272"
                     /clone_lib="NIH_MGC_12"
                     /tissue_type="cervical carcinoma cell line"
                     /lab_host="DH10B"
                     /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.4 kb. Library prepared by Life
                     Technologies."
BASE COUNT      138 a    197 c    180 g    182 t
ORIGIN

  Query Match             60.6%;  Score 20;  DB 13;  Length 697;
```

```
  Best Local Similarity   82.1%;  Pred. No. 3.2e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       6 CTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           || || ||||||||| || ||| |||||
Db     501 CTCGTGGACAAGAGTATGCCAGAGGGAG 528


RESULT 12
BH598122
LOCUS       BH598122                728 bp    DNA     linear   GSS 15-DEC-2001
DEFINITION  BOGLZ53TF BOGL Brassica oleracea genomic clone BOGLZ53, DNA
            sequence.
ACCESSION   BH598122
VERSION     BH598122.1  GI:17850574
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 728)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGLZ53TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .728
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGLZ53"
                     /clone_lib="BOGL"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      211 a    171 c    158 g    188 t
ORIGIN

  Query Match            60.6%;  Score 20;  DB 17;  Length 728;
  Best Local Similarity   82.1%;  Pred. No. 3.3e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGG 30
           | ||||| || |||| ||| ||||||||
Db     615 AATCTAGCCGTCAAGTGTTGGTCAGTGG 642


RESULT 13
BH449843
LOCUS       BH449843                833 bp    DNA     linear   GSS 12-DEC-2001
DEFINITION  BOGRE19TR BOGR Brassica oleracea genomic clone BOGRE19, DNA
            sequence.
ACCESSION   BH449843
VERSION     BH449843.1  GI:17635554
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 833)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGRE19TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .833
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGRE19"
                     /clone_lib="BOGR"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      152 a    226 c    214 g    241 t
ORIGIN

  Query Match            60.6%;  Score 20;  DB 17;  Length 833;
  Best Local Similarity   82.1%;  Pred. No. 3.6e+02;
  Matches   23;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTGG 30
           | ||||| || |||| ||| ||||||||
Db       8 AATCTAGCCGTCAAGTGTTGGTCAGTGG 35


RESULT 14
BM468802/c
LOCUS       BM468802                978 bp    mRNA    linear   EST 05-FEB-2002
DEFINITION  AGENCOURT_6445892 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:5587137
            5', mRNA sequence.
ACCESSION   BM468802
VERSION     BM468802.1  GI:18517844
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 978)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12356  row: c  column: 10
            High quality sequence start: 92
            High quality sequence stop: 260.
FEATURES             Location/Qualifiers
     source          1. .978
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5587137"
                     /clone_lib="NIH_MGC_92"
                     /tissue_type="embryonal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: testis; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 2.5 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      283 a    224 c    240 g    231 t
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ORIGIN

  Query Match            60.6%;  Score 20;  DB 13;  Length 978;
  Best Local Similarity  100.0%;  Pred. No. 3.9e+02;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      14 CAAGAGTTTGTCAGTGGGAG 33
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Db     785 CAAGAGTTTGTCAGTGGGAG 766


RESULT 15
BB150049/c
LOCUS       BB150049                240 bp    mRNA    linear   EST 28-JUN-2000
DEFINITION  BB150049 RIKEN full-length enriched, 6 days neonate skin Mus
            musculus cDNA clone A030003L20 3', mRNA sequence.
ACCESSION   BB150049
VERSION     BB150049.1  GI:8804986
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 240)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center(GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .240
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
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                     /clone_lib="RIKEN full-length enriched, 6 days neonate
                     skin"
                     /tissue_type="skin"
                     /dev_stage="6 days neonate"
                     /lab_host="DH10B"
                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3']. cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 10.0 and subtraction to Rot = 185.0. Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC I. "
BASE COUNT       65 a     43 c     47 g     85 t
ORIGIN

  Query Match            60.0%;  Score 19.8;  DB 10;  Length 240;
  Best Local Similarity  77.4%;  Pred. No. 2.2e+02;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGG 31
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Db      43 GCATTCTAGGGGCCAAGGATGTCTCAGTGGG 13


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Job time : 2433 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 10:54:58 ; Search time 32 Seconds
(without alignments)
407.819 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 33
Sequence: 1 gcattctagtcgacaagagtttgtcagtgggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	19.8	60.0	401	9	US-09-946-807-667	Sequence 667, App
c	3	19.8	60.0	401	10	US-09-795-668-666	Sequence 666, App
c	4	19.8	60.0	401	10	US-09-795-668-667	Sequence 667, App
c	5	19.8	60.0	401	10	US-09-795-686-666	Sequence 666, App
c	6	19.8	60.0	401	10	US-09-795-686-667	Sequence 667, App
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c	8	19.8	60.0	1503841	10	US-09-795-668-1	Sequence 1, Appli
c	9	19.8	60.0	1503841	10	US-09-795-686-1	Sequence 1, Appli
	10	18.6	56.4	709	10	US-09-960-253-137	Sequence 137, App
c	11	18.6	56.4	1732	9	US-10-063-547-81	Sequence 81, Appl
c	12	18.6	56.4	1732	12	US-10-006-867-81	Sequence 81, Appl
c	13	18.6	56.4	1732	12	US-10-052-586-281	Sequence 281, App
	14	18.6	56.4	3073	10	US-09-867-701-10910	Sequence 10910, A
	15	18.6	56.4	3073	10	US-09-920-300A-1690	Sequence 1690, Ap
	16	18.6	56.4	3073	12	US-10-033-528-1690	Sequence 1690, Ap
c	17	18.4	55.8	1311	10	US-09-964-824A-232	Sequence 232, App
c	18	18.4	55.8	1311	10	US-09-880-107-1617	Sequence 1617, Ap
	19	18.4	55.8	2484	10	US-09-839-497A-4	Sequence 4, Appli
c	20	18.4	55.8	148567	10	US-09-801-876B-3	Sequence 3, Appli
c	21	18.2	55.2	43058	10	US-09-954-456-292	Sequence 292, App
c	22	18.2	55.2	43058	10	US-09-954-456-529	Sequence 529, App
c	23	18.2	55.2	43058	10	US-09-880-107-3950	Sequence 3950, Ap
	24	18.2	55.2	659158	9	US-09-771-208-20	Sequence 20, Appl
	25	18	54.5	368	10	US-09-960-352-2011	Sequence 2011, Ap
c	26	18	54.5	1786	12	US-10-052-586-481	Sequence 481, App
	27	17.6	53.3	1803	10	US-09-801-368-157	Sequence 157, App
	28	17.6	53.3	1858	9	US-09-965-529-58	Sequence 58, Appl
	29	17.6	53.3	2000	9	US-09-938-842A-3773	Sequence 3773, Ap
c	30	17.6	53.3	152331	9	US-10-095-407-16	Sequence 16, Appl
	31	17.6	53.3	176373	9	US-10-095-407-17	Sequence 17, Appl
	32	17.4	52.7	196	10	US-09-878-574-9563	Sequence 9563, Ap
	33	17.4	52.7	404	10	US-09-728-446-1182	Sequence 1182, Ap
	34	17.4	52.7	5866	12	US-10-044-090-215	Sequence 215, App
c	35	17.2	52.1	144	10	US-09-864-761-18243	Sequence 18243, A
	36	17.2	52.1	382	10	US-09-770-791-163	Sequence 163, App
c	37	17.2	52.1	387	10	US-09-864-761-16334	Sequence 16334, A
c	38	17.2	52.1	470	10	US-09-864-761-1484	Sequence 1484, Ap
c	39	17.2	52.1	527	10	US-09-864-761-32816	Sequence 32816, A
c	40	17.2	52.1	657	9	US-09-938-842A-3874	Sequence 3874, Ap
	41	17.2	52.1	2895	9	US-09-938-842A-2540	Sequence 2540, Ap
	42	17.2	52.1	6319	10	US-09-995-494-58	Sequence 58, Appl
	43	17.2	52.1	32768	10	US-09-070-927A-17	Sequence 17, Appl
c	44	17	51.5	442	10	US-09-864-761-224	Sequence 224, App
c	45	17	51.5	442	10	US-09-864-761-225	Sequence 225, App

ALIGNMENTS

RESULT 1
US-09-946-807-666/c
; Sequence 666, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 666
; LENGTH: 401
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-666

Query Match 60.0%; Score 19.8; DB 9; Length 401;
Best Local Similarity 77.4%; Pred. No. 5.2;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
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RESULT 2
US-09-946-807-667/c
; Sequence 667, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE

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;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/946,807
;  CURRENT FILING DATE:  2001-09-05
;  PRIOR APPLICATION NUMBER: US/09/795,668
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 667
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-946-807-667

  Query Match             60.0%;  Score 19.8;  DB 9;  Length 401;
  Best Local Similarity   77.4%;  Pred. No. 5.2;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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Db     52 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 22


RESULT 3
US-09-795-668-666/c
; Sequence 666, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/795,668
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 666
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-668-666

  Query Match             60.0%;  Score 19.8;  DB 10;  Length 401;
  Best Local Similarity   77.4%;  Pred. No. 5.2;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
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Db    167 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 137


RESULT 4
US-09-795-668-667/c
; Sequence 667, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/795,668
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 667
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-668-667

  Query Match             60.0%;  Score 19.8;  DB 10;  Length 401;
  Best Local Similarity   77.4%;  Pred. No. 5.2;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          | || |||||  ||| |  ||||||||||||
Db     52 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 22


RESULT 5
US-09-795-686-666/c
; Sequence 666, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2005-001
;  CURRENT APPLICATION NUMBER: US/09/795,686
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,715
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 666
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-686-666

  Query Match             60.0%;  Score 19.8;  DB 10;  Length 401;
  Best Local Similarity   77.4%;  Pred. No. 5.2;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
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Db    167 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 137


RESULT 6
US-09-795-686-667/c
; Sequence 667, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2005-001
;  CURRENT APPLICATION NUMBER: US/09/795,686
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,715
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 667
;   LENGTH: 401
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-686-667

  Query Match             60.0%;  Score 19.8;  DB 10;  Length 401;
  Best Local Similarity   77.4%;  Pred. No. 5.2;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          | || |||||  ||| |  ||||||||||||
Db     52 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 22
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RESULT 7
US-09-946-807-1/c
; Sequence 1, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/946,807
;  CURRENT FILING DATE:  2001-09-05
;  PRIOR APPLICATION NUMBER: US/09/795,668
;  PRIOR FILING DATE: 2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: r=g or a
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: y=t/u or c
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;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: m=a or c
;   FEATURE:
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;   LOCATION: (1)...(1531)
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;   FEATURE:
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;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: s=g or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: w=a or t/u
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: b=g or c or t/u
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: d=a or g or t/u
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: h=a or c or t/u
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: v=a or g or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: n=a or g or c or t/u
US-09-946-807-1

  Query Match             60.0%;  Score 19.8;  DB 9;  Length 1503841;
  Best Local Similarity   77.4%;  Pred. No. 27;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           | || |||||  ||| |  ||||||||||||
Db 815361 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 815331


RESULT 8
US-09-795-668-1/c
; Sequence 1, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/795,668
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1503841
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: r=g or a
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: y=t/u or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: m=a or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: k=g or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: s=g or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: w=a or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: b=g or c or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: d=a or g or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: h=a or c or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: v=a or g or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: n=a or g or c or t/u
US-09-795-668-1

  Query Match             60.0%;  Score 19.8;  DB 10;  Length 1503841;
  Best Local Similarity   77.4%;  Pred. No. 27;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           | || |||||  ||| |  ||||||||||||
Db 815361 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 815331


RESULT 9
US-09-795-686-1/c
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; Sequence 1, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2005-001
;  CURRENT APPLICATION NUMBER: US/09/795,686
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,715
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1503841
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: r=g or a
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: y=t/u or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: m=a or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: k=g or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: s=g or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: w=a or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: b=g or c or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: d=a or g or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: h=a or c or t/u
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: v=a or g or c
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(1531)
;   OTHER INFORMATION: n=a or g or c or t/u
US-09-795-686-1

  Query Match           60.0%;  Score 19.8;  DB 10;  Length 1503841;
  Best Local Similarity   77.4%;  Pred. No. 27;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           | || |||||  ||| |  ||||||||||||
Db  815361 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 815331


RESULT 10
US-09-960-253-137
; Sequence 137, Application US/09960253
; Patent No. US20020123619A1
; GENERAL INFORMATION:
;  APPLICANT: Benson, Darin R.
;  APPLICANT:  Mohamath, Raodoh
;  APPLICANT:  Lodes, Michael J.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; cTITLE OF INVENTION:  AND DIAGNOSIS OF LUNG CANCER
;  FILE REFERENCE: 210121.556
;  CURRENT APPLICATION NUMBER: US/09/960,253
;  CURRENT FILING DATE:  2001-09-20
;  NUMBER OF SEQ ID NOS: 187
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
;   LENGTH: 709
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-960-253-137

  Query Match           56.4%;  Score 18.6;  DB 10;  Length 709;
  Best Local Similarity   84.0%;  Pred. No. 21;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGT 28
           |||||| ||  | ||||||||||||
Db     606 TTCTAGGCGTGAGGAGTTTGTCAGT 630


RESULT 11
US-10-063-547-81/c
; Sequence 81, Application US/10063547
; Publication No. US20020182638A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
;  CURRENT APPLICATION NUMBER: US/10/063,547
;  CURRENT FILING DATE:  2002-05-02
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 81
;   LENGTH: 1732
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-10-063-547-81

  Query Match           56.4%;  Score 18.6;  DB 9;  Length 1732;
  Best Local Similarity   72.7%;  Pred. No. 25;
  Matches   24;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           |||  || | |  || |||| || |||||||||
Db     808 GCAGGCTTGGCAGCAGGAGTCTGGCAGTGGGAG 776


RESULT 12
US-10-006-867-81/c
; Sequence 81, Application US/10006867
; Patent No. US20020119130A1
; GENERAL INFORMATION:
;  APPLICANT: Eaton,Dan L.
;  APPLICANT:  Filvaroff,Ellen
;  APPLICANT:  Gerritsen,Mary E.
;  APPLICANT:  Goddard,Audrey
;  APPLICANT:  Godowski,Paul J.
;  APPLICANT:  Grimaldi,Christopher J.
;  APPLICANT:  Gurney,Austin L.
;  APPLICANT:  Watanabe,Colin K.
;  APPLICANT:  Wood,William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3230R1C1
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; CURRENT APPLICATION NUMBER: US/10/006,867
; CURRENT FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/063435
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/064215
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083495
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088030
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; PRIOR APPLICATION NUMBER: 60/103449
; PRIOR FILING DATE: 1998-10-06
; PRIOR APPLICATION NUMBER: 60/103678
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103679
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/103711
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 60/105000
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; PRIOR APPLICATION NUMBER: 60/105881
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; PRIOR FILING DATE: 1998-10-28
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; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 60/106856
; PRIOR FILING DATE: 1998-11-03
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; PRIOR APPLICATION NUMBER: 60/113408
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621
; PRIOR FILING DATE: 1998-12-23
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; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 60/115614
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116527
; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/119285
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119287
; PRIOR FILING DATE: 1999-02-09
; PRIOR APPLICATION NUMBER: 60/119525
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/119549
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: 60/120014
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/129674
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/175481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/199397
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380142

Query Match 56.4%; Score 18.6; DB 12; Length 1732;
Best Local Similarity 72.7%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
          |||  || | |  || |||| || |||||||||
Db    808 GCAGGCTTGGCAGCAGGAGTCTGGCAGTGGGAG 776
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RESULT 13
US-10-052-586-281/c
; Sequence 281, Application US/10052586
; Patent No. US20020127584A1
; GENERAL INFORMATION:
; APPLICANT: Baker,Kevin P.
; APPLICANT: Chen,Jian
; APPLICANT: Desnoyers,Luc
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Pan,James
; APPLICANT: Smith,Victoria
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT APPLICATION NUMBER: US/10/052,586
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
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; PRIOR FILING DATE: 1997-10-21
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; PRIOR FILING DATE: 1997-10-28
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; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
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; PRIOR APPLICATION NUMBER: 60/080327
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; PRIOR FILING DATE: 1998-04-01
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
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; PRIOR APPLICATION NUMBER: 60/088861
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; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089908

Query Match 56.4%; Score 18.6; DB 12; Length 1732;
Best Local Similarity 72.7%; Pred. No. 25;
Matches 24; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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RESULT 14
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; Sequence 10910, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10910
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10910

Query Match 56.4%; Score 18.6; DB 10; Length 3073;
Best Local Similarity 84.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 15

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US-09-920-300A-1690
; Sequence 1690, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1690
;   LENGTH: 3073
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1690

  Query Match             56.4%;  Score 18.6;  DB 10;  Length 3073;
  Best Local Similarity   84.0%;  Pred. No. 28;
  Matches   21;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGT 28
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Db     606 TTCTAGGCGTGAGGAGTTTGTCAGT 630

Search completed: December 16, 2002, 11:13:13
Job time : 998 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 10:54:58 ; Search time 302 Seconds
(without alignments)
246.079 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 33
Sequence: 1 gcattctagtcgacaagagtttgtcagtgggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	19.8	60.0	401	22	AAK95867	Human neuregulin g
c	2	19.8	60.0	401	22	AAK95868	Human neuregulin g
c	3	19.8	60.0	401	22	AAK97360	Human neuregulin g
c	4	19.8	60.0	401	22	AAK97361	Human neuregulin g
c	5	19.8	60.0	1715	23	ABL29013	Drosophila melanog
	6	19.8	60.0	3792	23	ABL29012	Drosophila melanog
c	7	19.8	60.0	1503900	22	AAK95240	Human neuregulin-1
c	8	19.8	60.0	1503900	22	AAK96733	Human neuregulin-1
c	9	19.2	58.2	731	21	AAC43835	Arabidopsis thalia
	10	19.2	58.2	782	23	AAS74037	DNA encoding novel
	11	19.2	58.2	16236	24	ABL33023	Human immune syste
c	12	19	57.6	1177	9	AAN81277	New sequence of ra
c	13	19	57.6	1177	17	AAT18809	Type I (beta-1) ra
c	14	19	57.6	1802	9	AAN82021	Sequence encoding
c	15	19	57.6	2600	10	AAN90750	Protein kinase C b
c	16	19	57.6	3202	17	AAQ74001	Type I (beta-1) ra
c	17	19	57.6	3418	9	AAN81279	Entire nucleotide
c	18	19	57.6	3418	17	AAT15006	Type II (beta-2) r
c	19	19	57.6	4829	20	AAZ35666	Ovine interferon g
c	20	19	57.6	4842	20	AAZ35665	Ovine interferon g
c	21	18.8	57.0	925	21	AAC37620	Arabidopsis thalia
c	22	18.8	57.0	1331	21	AAC39790	Arabidopsis thalia
c	23	18.8	57.0	1465	21	AAC51439	Arabidopsis thalia
	24	18.8	57.0	6081	24	ABN80193	Human chemically m
	25	18.8	57.0	6081	24	ABL33429	Human immune syste
c	26	18.6	56.4	666	24	ABQ60322	Human colon cancer
	27	18.6	56.4	709	24	ABK70266	Human lung cancer
	28	18.6	56.4	824	22	AAI93936	Human neuroblastom
c	29	18.6	56.4	1720	22	AAC84305	Human EXCS encodin
c	30	18.6	56.4	1731	22	AAS46065	Human DNA encoding
c	31	18.6	56.4	1732	21	AAA37064	Human PRO1557 (UNQ
c	32	18.6	56.4	1732	22	AAF92098	Human PRO1557 cDNA
c	33	18.6	56.4	1732	22	AAF54300	DNA encoding prote
c	34	18.6	56.4	1738	24	ABK12126	Human cDNA encodin
	35	18.6	56.4	2639	23	ABL02633	Drosophila melanog
	36	18.6	56.4	3073	24	ABK46139	cDNA encoding colo
	37	18.6	56.4	3073	24	ABL87932	Human ovarian canc
	38	18.6	56.4	4945	23	ABL02632	Drosophila melanog
	39	18.6	56.4	5669	22	AAK70832	Human immune/haema
c	40	18.6	56.4	17450	22	AAL05953	Human reproductive
	41	18.6	56.4	17450	22	AAK70834	Human immune/haema
c	42	18.6	56.4	17450	23	ABL98517	Human testicular a
c	43	18.4	55.8	60	24	ABN36300	Human spliced tran
	44	18.4	55.8	445	20	AAX51871	Human secreted pro
	45	18.4	55.8	460	20	AAX51869	Human secreted pro

ALIGNMENTS

RESULT 1
AAK95867/c
ID AAK95867 standard; DNA; 401 BP.
XX
AC AAK95867;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG815395.
XX
KW Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
KW gene therapy; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
PN WO200164876-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06376.
XX
PR 28-FEB-2000; 2000US-0515715.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson H, Steinthorsdottir V, Gulcher JR;
XX
DR WPI; 2001-550179/61.
XX
PT Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
PT preventing diagnosing and treating schizophrenia -
XX

PS Disclosure; Page 609; 750pp; English.
XX
CC This sequence represents a single nucleotide polymorphism (SNP) of the
CC human neuregulin-1 associated gene 1 (NRG1AG1) of the invention. The
CC NRG1AG1 gene is also referred to as the human Schizophrenia gene. The
CC invention also relates to fragments or variants of the gene and the
CC NRG1AG1 polypeptides they encode. The NRG1AG1 nucleic acids and
CC polypeptides may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate NRG1AG1 expression. For example,
CC they may be used to treat disorders associated with decreased expression
CC by rectifying mutations or deletions in a patient's genome that affect
CC the activity of NRG1AG1 by expressing inactive proteins or to supplement
CC the patients own production of NRG1AG1. Additionally, the gene may be
CC used to produce NRG1AG1 polypeptides, by inserting the nucleic acids into
CC a host cell and culturing the cell to express the protein. The gene may
CC also be used as DNA probes and primers in diagnostic assays to detect and
CC quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC NRG1AG1 polypeptides may also be used as antigens in the production of
CC antibodies against NRG1AG1 and in assays to identify modulators of
CC NRG1AG1 expression and activity. Anti-NRG1AG1 antibodies and antagonists
CC may also be used to down regulate expression and activity. Anti-NRG1AG1
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of NRG1AG1 polypeptides in samples. NRG1AG1 Is associated with
CC schizophrenia which may be prevented, diagnosed and/or treated by the
CC above methods.
XX
SQ Sequence 401 BP; 138 A; 91 C; 67 G; 103 T; 2 other;

Query Match 60.0%; Score 19.8; DB 22; Length 401;
Best Local Similarity 77.4%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
| || ||||| ||| | ||||||||||||
Db 167 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 137

RESULT 2
AAK95868/c
ID AAK95868 standard; DNA; 401 BP.
XX
AC AAK95868;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG815510.
XX
KW Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
KW gene therapy; single nucleotide polymorphism; SNP; ds.
XX
OS Homo sapiens.
XX
PN WO200164876-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06376.
XX
PR 28-FEB-2000; 2000US-0515715.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson H, Steinthorsdottir V, Gulcher JR;
XX
DR WPI; 2001-550179/61.
XX
PT Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
PT preventing diagnosing and treating schizophrenia -
XX
PS Disclosure; Page 609; 750pp; English.
XX
CC This sequence represents a single nucleotide polymorphism (SNP) of the
CC human neuregulin-1 associated gene 1 (NRG1AG1) of the invention. The
CC NRG1AG1 gene is also referred to as the human Schizophrenia gene. The
CC invention also relates to fragments or variants of the gene and the
CC NRG1AG1 polypeptides they encode. The NRG1AG1 nucleic acids and
CC polypeptides may be used in the prevention, diagnosis and treatment of
CC diseases associated with inappropriate NRG1AG1 expression. For example,
CC they may be used to treat disorders associated with decreased expression
CC by rectifying mutations or deletions in a patient's genome that affect
CC the activity of NRG1AG1 by expressing inactive proteins or to supplement
CC the patients own production of NRG1AG1. Additionally, the gene may be
CC used to produce NRG1AG1 polypeptides, by inserting the nucleic acids into
CC a host cell and culturing the cell to express the protein. The gene may
CC also be used as DNA probes and primers in diagnostic assays to detect and
CC quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC NRG1AG1 polypeptides may also be used as antigens in the production of
CC antibodies against NRG1AG1 and in assays to identify modulators of
CC NRG1AG1 expression and activity. Anti-NRG1AG1 antibodies and antagonists
CC may also be used to down regulate expression and activity. Anti-NRG1AG1
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of NRG1AG1 polypeptides in samples. NRG1AG1 Is associated with
CC schizophrenia which may be prevented, diagnosed and/or treated by the
CC above methods.
XX
SQ Sequence 401 BP; 133 A; 99 C; 71 G; 95 T; 3 other;

Query Match 60.0%; Score 19.8; DB 22; Length 401;
Best Local Similarity 77.4%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
| || ||||| ||| | ||||||||||||
Db 52 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 22

RESULT 3
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ID AAK97360 standard; DNA; 401 BP.
XX
AC AAK97360;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG815395.
XX
KW Human; neuregulin 1 gene; schizophrenia; gene therapy; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200164877-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06377.
XX
PR 28-FEB-2000; 2000US-0515716.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson H, Steinthorsdottir V, Gulcher JR;
XX
DR WPI; 2001-514841/56.
XX
PT Neuregulin 1 nucleic acids and proteins useful for diagnosing
PT preventing and treating schizophrenia -
XX
PS Disclosure; Page 194; 756pp; English.
XX
CC This sequence represents a single nucleotide polymorphism (SNP)
CC from the human neuregulin 1 gene of the invention.
CC The invention also relates to fragments or variants of the neuregulin 1
CC gene. The gene and its proteins may be used in the prevention, diagnosis

CC and treatment of diseases associated with inappropriate neuregulin 1
CC expression, such as schizophrenia. For example they may be used to treat
CC disorders associated with decreased neuregulin 1 expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC neuregulin 1 by expressing inactive proteins or to supplement the
CC patients own production of polypeptides. Additionally, the gene may be
CC used to produce the neuregulin 1 protein, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The gene
CC and its complementary sequences may also be used as DNA probes in
CC diagnostic assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. The protein may also be used as antigens in the
CC production of antibodies against neuregulin 1 and in assays to identify
CC modulators of neuregulin 1 expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of neuregulin 1 in samples.
XX
SQ Sequence 401 BP; 138 A; 91 C; 67 G; 103 T; 2 other;

Query Match 60.0%; Score 19.8; DB 22; Length 401;
Best Local Similarity 77.4%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
| || ||||| ||| | ||||||||||||
Db 167 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 137

RESULT 4
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ID AAK97361 standard; DNA; 401 BP.
XX
AC AAK97361;
XX
DT 17-DEC-2001 (first entry)
XX
DE Human neuregulin gene single nucleotide polymorphism SNP8NRG815510.
XX
KW Human; neuregulin 1 gene; schizophrenia; gene therapy; SNP;
KW single nucleotide polymorphism; ds.
XX
OS Homo sapiens.
XX
PN WO200164877-A2.
XX
PD 07-SEP-2001.
XX
PF 28-FEB-2001; 2001WO-US06377.
XX
PR 28-FEB-2000; 2000US-0515716.
XX
PA (DECO-) DECODE GENETICS EHF.
XX
PI Stefansson H, Steinthorsdottir V, Gulcher JR;
XX
DR WPI; 2001-514841/56.
XX
PT Neuregulin 1 nucleic acids and proteins useful for diagnosing
PT preventing and treating schizophrenia -
XX
PS Disclosure; Page 194; 756pp; English.
XX
CC This sequence represents a single nucleotide polymorphism (SNP)
CC from the human neuregulin 1 gene of the invention.
CC The invention also relates to fragments or variants of the neuregulin 1
CC gene. The gene and its proteins may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate neuregulin 1
CC expression, such as schizophrenia. For example they may be used to treat
CC disorders associated with decreased neuregulin 1 expression by rectifying
CC mutations or deletions in a patient's genome that affect the activity of
CC neuregulin 1 by expressing inactive proteins or to supplement the
CC patients own production of polypeptides. Additionally, the gene may be
CC used to produce the neuregulin 1 protein, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the protein. The gene
CC and its complementary sequences may also be used as DNA probes in
CC diagnostic assays to detect and quantitate the presence of similar
CC nucleic acids in samples, and therefore which patients may be in need of
CC restorative therapy. The protein may also be used as antigens in the
CC production of antibodies against neuregulin 1 and in assays to identify
CC modulators of neuregulin 1 expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity.
CC The antibodies may also be used as diagnostic agents for detecting the
CC presence of neuregulin 1 in samples.
XX
SQ Sequence 401 BP; 133 A; 99 C; 71 G; 95 T; 3 other;

Query Match 60.0%; Score 19.8; DB 22; Length 401;
Best Local Similarity 77.4%; Pred. No. 18;
Matches 24; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
| || ||||| ||| | ||||||||||||
Db 52 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 22

RESULT 5
ABL29013/c
ID ABL29013 standard; DNA; 1715 BP.
XX
AC ABL29013;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38512.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 38512; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 1715 BP; 436 A; 426 C; 460 G; 393 T; 0 other;

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  Query Match            60.0%;  Score 19.8;  DB 23;  Length 1715;
  Best Local Similarity   77.4%;  Pred. No. 24;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          |||| | || ||||||| || ||| |||| |
Db    842 CATTATGGTGGACAAGATTTCGTCGGTGGCA 812


RESULT 6
ABL29012
ID   ABL29012 standard; DNA; 3792 BP.
XX
AC   ABL29012;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 38509.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 38509; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3792 BP; 1016 A; 905 C; 846 G; 1025 T; 0 other;

  Query Match            60.0%;  Score 19.8;  DB 23;  Length 3792;
  Best Local Similarity   77.4%;  Pred. No. 28;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          |||| | || ||||||| || ||| |||| |
Db   1951 CATTATGGTGGACAAGATTTCGTCGGTGGCA 1981


RESULT 7
AAK95240/c
ID   AAK95240 standard; DNA; 1503900 BP.
XX
AC   AAK95240;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Human neuregulin-1 gene.
XX
KW   Human; neuregulin-1 associated gene 1; NRG1AG1; Schizophrenia gene;
KW   gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200164876-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06376.
XX
PR   28-FEB-2000; 2000US-0515715.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Stefansson H,  Steinthorsdottir V,  Gulcher JR;
XX
DR   WPI; 2001-550179/61.
DR   P-PSDB; AAG67900, AAG67901, AAG67902, AAG67903, AAG67904, AAG67905,
DR   AAG67906, AAG67907, AAG67908, AAG67909, AAG67910, AAG67911, AAG67912,
DR   AAG67913, AAG67914, AAG67915, AAG67916, AAG67917, AAG67918, AAG67919,
DR   AAG67920, AAG67921, AAG67922, AAG67923, AAG67924, AAG67925, AAG67926,
DR   AAG67927, AAG67928, AAG67929, AAG67930, AAG67931, AAG67932, AAG67933,
DR   AAG67934, AAG67935, AAG67936, AAG67937.
XX
PT   Neuregulin-1 associated gene 1 nucleic acids and fragments, useful for
PT   preventing diagnosing and treating schizophrenia -
XX
PS   Disclosure; Page 90-501; 750pp; English.
XX
CC   This sequence represents the human neuregulin-1 associated gene 1
CC   (NRG1AG1) of the invention. The NRG1AG1 gene is also referred to as the
CC   human Schizophrenia gene. The invention also relates to fragments or
CC   variants of the gene and the NRG1AG1 polypeptides they encode. The
CC   NRG1AG1 nucleic acids and polypeptides may be used in the prevention,
CC   diagnosis and treatment of diseases associated with inappropriate NRG1AG1
CC   expression. For example, they may be used to treat disorders associated
CC   with decreased expression by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of NRG1AG1 by expressing
CC   inactive proteins or to supplement the patients own production of
CC   NRG1AG1. Additionally, the gene may be used to produce NRG1AG1
CC   polypeptides, by inserting the nucleic acids into a host cell and
CC   culturing the cell to express the protein. The gene may also be used as
CC   DNA probes and primers in diagnostic assays to detect and quantitate the
CC   presence of similar nucleic acids in samples, and therefore which
CC   patients may be in need of restorative therapy. The NRG1AG1 polypeptides
CC   may also be used as antigens in the production of antibodies against
CC   NRG1AG1 and in assays to identify modulators of NRG1AG1 expression and
CC   activity. Anti-NRG1AG1 antibodies and antagonists may also be used to
CC   down regulate expression and activity. Anti-NRG1AG1 antibodies may
CC   also be used as diagnostic agents for detecting the presence of NRG1AG1
CC   polypeptides in samples. NRG1AG1 Is associated with schizophrenia which
CC   may be prevented, diagnosed and/or treated by the above methods.
XX
SQ   Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;

  Query Match            60.0%;  Score 19.8;  DB 22;  Length 1503900;
  Best Local Similarity   77.4%;  Pred. No. 99;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          | || |||||  ||| |  ||||||||||||
Db 815360 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 815330


RESULT 8
AAK96733/c
ID   AAK96733 standard; DNA; 1503900 BP.
```

```
XX
AC   AAK96733;
XX
DT   17-DEC-2001  (first entry)
XX
DE   Human neuregulin-1 gene.
XX
KW   Human; neuregulin 1 gene; schizophrenia; gene therapy; ds.
XX
OS   Homo sapiens.
XX
PN   WO200164877-A2.
XX
PD   07-SEP-2001.
XX
PF   28-FEB-2001; 2001WO-US06377.
XX
PR   28-FEB-2000; 2000US-0515716.
XX
PA   (DECO-) DECODE GENETICS EHF.
XX
PI   Stefansson H,  Steinthorsdottir V,  Gulcher JR;
XX
DR   WPI; 2001-514841/56.
DR   P-PSDB; AAG67938, AAG67939, AAG67940, AAG67941, AAG67942, AAG67943,
DR   AAG67944, AAG67945, AAG67946, AAG67947, AAG67948, AAG67949,
DR   AAG67950, AAG67951, AAG67952, AAG67953, AAG67954, AAG67955,
DR   AAG67956, AAG67957, AAG67958, AAG67959, AAG67960, AAG67961,
DR   AAG67962, AAG67963, AAG67964, AAG67965, AAG67966, AAG67967,
DR   AAG67968, AAG67969, AAG67970, AAG67971, AAG67972, AAG67973,
DR   AAG67974, AAG67975.
XX
PT   Neuregulin 1 nucleic acids and proteins useful for diagnosing
PT   preventing and treating schizophrenia -
XX
PS   Disclosure; Page 345-756; 756pp; English.
XX
CC   This sequence represents the human neuregulin 1 gene of the invention.
CC   The invention also relates to fragments or variants of the neuregulin 1
CC   gene. The gene and its proteins may be used in the prevention, diagnosis
CC   and treatment of diseases associated with inappropriate neuregulin 1
CC   expression, such as schizophrenia. For example they may be used to treat
CC   disorders associated with decreased neuregulin 1 expression by rectifying
CC   mutations or deletions in a patient's genome that affect the activity of
CC   neuregulin 1 by expressing inactive proteins or to supplement the
CC   patients own production of polypeptides. Additionally, the gene may be
CC   used to produce the neuregulin 1 protein, by inserting the nucleic acids
CC   into a host cell and culturing the cell to express the protein. The gene
CC   and its complementary sequences may also be used as DNA probes in
CC   diagnostic assays to detect and quantitate the presence of similar
CC   nucleic acids in samples, and therefore which patients may be in need of
CC   restorative therapy. The protein may also be used as antigens in the
CC   production of antibodies against neuregulin 1 and in assays to identify
CC   modulators of neuregulin 1 expression and activity. The antibodies and
CC   antagonists may also be used to down regulate expression and activity.
CC   The antibodies may also be used as diagnostic agents for detecting the
CC   presence of neuregulin 1 in samples.
XX
SQ   Sequence 1503900 BP; 452487 A; 281874 C; 288074 G; 480092 T; 1373 other;

  Query Match             60.0%;  Score 19.8;  DB 22;  Length 1503900;
  Best Local Similarity   77.4%;  Pred. No. 99;
  Matches   24;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           | || |||||  ||| |  ||||||||||||
Db 815360 CCTTTTAGTCTTCAACAAATTGTCAGTGGGA 815330


RESULT 9
AAC43835/c
ID   AAC43835 standard; DNA; 731 BP.
XX
AC   AAC43835;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana DNA fragment SEQ ID NO: 40686.
XX
KW   Hybridisation assay; genetic mapping; gene expression control;
KW   protein identification; signal transduction pathway;
KW   metabolic pathway; promoter; termination sequence; ss.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;   99US-0121825.
PR   05-MAR-1999;   99US-0123180.
PR   09-MAR-1999;   99US-0123548.
PR   23-MAR-1999;   99US-0125788.
PR   25-MAR-1999;   99US-0126264.
PR   29-MAR-1999;   99US-0126785.
PR   01-APR-1999;   99US-0127462.
PR   06-APR-1999;   99US-0128234.
PR   08-APR-1999;   99US-0128714.
PR   16-APR-1999;   99US-0129845.
PR   19-APR-1999;   99US-0130077.
PR   21-APR-1999;   99US-0130449.
PR   23-APR-1999;   99US-0130510.
PR   23-APR-1999;   99US-0130891.
PR   28-APR-1999;   99US-0131449.
PR   30-APR-1999;   99US-0132048.
PR   30-APR-1999;   99US-0132407.
PR   04-MAY-1999;   99US-0132484.
PR   05-MAY-1999;   99US-0132485.
PR   06-MAY-1999;   99US-0132486.
PR   06-MAY-1999;   99US-0132487.
PR   07-MAY-1999;   99US-0132863.
PR   11-MAY-1999;   99US-0134256.
PR   14-MAY-1999;   99US-0134218.
PR   14-MAY-1999;   99US-0134219.
PR   14-MAY-1999;   99US-0134221.
PR   14-MAY-1999;   99US-0134370.
PR   18-MAY-1999;   99US-0134768.
PR   19-MAY-1999;   99US-0134941.
PR   20-MAY-1999;   99US-0135124.
PR   21-MAY-1999;   99US-0135353.
PR   24-MAY-1999;   99US-0135629.
PR   25-MAY-1999;   99US-0136021.
PR   27-MAY-1999;   99US-0136392.
PR   28-MAY-1999;   99US-0136782.
PR   01-JUN-1999;   99US-0137222.
PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
PR   16-JUN-1999;   99US-0139452.
PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
PR   18-JUN-1999;   99US-0139459.
PR   18-JUN-1999;   99US-0139460.
PR   18-JUN-1999;   99US-0139461.
PR   18-JUN-1999;   99US-0139462.
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PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 58.2%; Score 19.2; DB 21; Length 731;
Best Local Similarity 87.5%; Pred. No. 38;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      3 ATTCTAGTCGACAAGAGTTTGTCA 26
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Db    477 ATTGTAGTCAACAAGAGTTTGCCA 454
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RESULT 10
AAS74037
ID AAS74037 standard; cDNA; 782 BP.
XX
AC AAS74037;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #9841.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

```
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG09850.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity  -
XX
PS   Claim 1; SEQ ID No 9841; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 782 BP; 177 A; 217 C; 243 G; 145 T; 0 other;

  Query Match            58.2%;  Score 19.2;  DB 23;  Length 782;
  Best Local Similarity  75.0%;  Pred. No. 39;
  Matches   24;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           | ||| ||||| || || ||  | ||||||||
Db     562 CCTTCCAGTCGCCAGGAATTCCTTAGTGGGAG 593


RESULT 11
ABL33023
ID   ABL33023 standard; DNA; 16236 BP.
XX
AC   ABL33023;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human immune system associated gene SEQ ID NO: 996.
XX
KW   Human; immune system disease; cytosine methylation; antiasthmatic;
KW   antiarteriosclerotic; antianaemic; cytostatic; nootropic;
KW   neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW   antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW   antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW   acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW   neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200200928-A2.
XX
PD   03-JAN-2002.
XX
PF   02-JUL-2001; 2001WO-EP07537.
XX
PR   30-JUN-2000; 2000DE-1032529.
PR   01-SEP-2000; 2000DE-1043826.
XX
PA   (EPIG-) EPIGENOMICS AG.
XX
PI   Olek A,  Piepenbrock C,  Berlin K;
XX
DR   WPI; 2002-130909/17.
XX
PT   Nucleic acid comprising fragment of chemically modified gene, useful
PT   for diagnosis and treatment of diseases associated with abnormal
PT   cytosine methylation  -
XX
PS   Claim 1; SEQ ID NO 996; 32pp + Sequence Listing; German.
XX
CC   The present invention provides a number of human immune system associated
CC   genes which are modified by the methylation of cytosines. The sequences
CC   can be used in the diagnosis and treatment of immune system disorders,
CC   including eye diseases such as retinopathy, neovascular glaucoma and
CC   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC   leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC   rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC   diseases. The present sequence is a gene of the invention.
XX
SQ   Sequence 16236 BP; 4368 A; 355 C; 3510 G; 8003 T; 0 other;

  Query Match            58.2%;  Score 19.2;  DB 24;  Length 16236;
  Best Local Similarity  75.0%;  Pred. No. 74;
  Matches   24;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
             | | | |||| || ||| |||||| ||| |||
Db    6084 GGAATGTAGTGGATAAGTGTTTGTGAGTTGGA 6115


RESULT 12
AAN81277/c
ID   AAN81277 standard; cDNA; 1177 BP.
XX
AC   AAN81277;
XX
DT   24-OCT-1990  (first entry)
XX
DE   New sequence of rat protein kinase C cDNA.
XX
KW   Rat kinase protein C cDNA; enzyme; EC-2.7.1.37; pTB638; ss.
XX
OS   Rat.
XX
FH   Key             Location/Qualifiers
FT   mat_peptide     1..675
FT                   /*tag=  a
FT   polyA_signal    1156..1161
FT                   /*tag=  b
FT   polyA_site      1177
FT                   /*tag=  c
XX
PN   EP251244-A.
XX
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PD   07-JAN-1988.
XX
PF   26-JUN-1987;   87EP-0109223.
XX
PR   25-FEB-1987;   87JP-0040160.
PR   27-JUN-1986;   86JP-0149385.
XX
PA   (TAKE ) TAKEDA CHEMICAL IND KK.
XX
PI   Ono Y,  Kurokawa T,  Igarashi K,  Nishizuka Y;
XX
DR   WPI; 1988-001173/01.
DR   P-PSDB; AAP80695.
XX
PT   New human and rat protein kinase C -
PT   for studying cellular signal transductor mechanisms
XX
PS   Example; Fig 2.1 - 2.2; 32pp; English.
XX
CC   The SQ is from a rat brain mRNA-derived cDNA library. It is contained in
CC   plasmid pTB638. AA sequences of the peptides nos. 24 and 51 determined
CC   in Kikkawa [J. Biol. Chem 257, 1334 (1982)] stictly corresp. to the
CC   nucleotide sequences at nos. 445-480 and 220-312, respectively. Thus, the
CC   plasmid pTB638 was confirmed to be rat protein kinase C cDNA.
XX
SQ   Sequence 1177 BP; 319 A; 244 C; 277 G; 337 T; 0 other;

  Query Match             57.6%;  Score 19;  DB 9;  Length 1177;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 AAGAGTTTGTCAGTGGGAG 33
           |||||||||||||||||||
Db     602 AAGAGTTTGTCAGTGGGAG 584


RESULT 13
AAT18809/c
ID   AAT18809 standard; cDNA; 1177 BP.
XX
AC   AAT18809;
XX
DT   07-AUG-1996  (first entry)
XX
DE   Type I (beta-1) rat brain protein kinase C partial cDNA.
XX
KW   Protein kinase C; signal transduction; tumour; diagnosis; therapy;
KW   ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..675
FT                   /*tag= a
FT   polyA_signal    1156..1161
FT                   /*tag= b
FT   misc_difference 1177
FT                   /*tag= c
FT                   /note= "base n at position 1177 signifies an
FT                          unspecified number of adenine bases"
XX
PN   EP686695-A1.
XX
PD   13-DEC-1995.
XX
PF   26-JUN-1987;   87EP-0112109.
XX
PR   25-FEB-1987;   87JP-0040160.
PR   27-JUN-1986;   86JP-0149385.
PR   18-SEP-1986;   86JP-0217944.
PR   28-NOV-1986;   86JP-0281870.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Igarashi K,  Kurokawa T,  Nishizuka Y,  Ono Y;
XX
DR   WPI; 1996-021913/03.
DR   P-PSDB; AAR94951.
XX
PT   New isolated rat protein kinase C - used to develop prods. for the
PT   study, diagnosis, prevention and treatment of diseases involving
PT   abnormal signal transduction
XX
PS   Example 2; Fig 2; 39pp; English.
XX
CC   A cDNA sequence (AAT18809) codes for a C-terminal portion (AAR94951)
CC   of type I (beta-1) rat brain protein kinase C (PKC), a protein that
CC   performs the transduction of extracellular signals into cells through
CC   the phosphorylation of proteins.  It was obtd. from a rat brain-
CC   derived cDNA library by screening with probes (see also AAT18806-08)
CC   based on isolated peptides of PKC.  A PstI fragment of the cDNA clone
CC   was used to screen a rat brain cDNA library, resulting in the
CC   identification of full-length sequences (see also AAQ74001 and AAT15006)
CC   coding for type I (AAR94953) and type II (AAR94764) PKC.
XX
SQ   Sequence 1177 BP; 318 A; 244 C; 277 G; 337 T; 1 other;

  Query Match             57.6%;  Score 19;  DB 17;  Length 1177;
  Best Local Similarity   100.0%;  Pred. No. 53;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 AAGAGTTTGTCAGTGGGAG 33
           |||||||||||||||||||
Db     602 AAGAGTTTGTCAGTGGGAG 584


RESULT 14
AAN82021/c
ID   AAN82021 standard; DNA; 1802 BP.
XX
AC   AAN82021;
XX
DT   16-OCT-1990  (first entry)
XX
DE   Sequence encoding protein kinase C-III (PKC-III).
XX
KW   Protein kinase C; PKC; cancer; ds.
XX
OS   Rattus sp.
XX
PN   WO8801303-A.
XX
PD   25-FEB-1988.
XX
PF   13-AUG-1987;   87WO-0002005.
XX
PR   13-AUG-1986;   86US-0896476.
XX
PA   (GENE-) GENETICS INST INC.
XX
PI   Knopf JL;
XX
DR   WPI; 1988-064018/09.
DR   P-PSDB; AAP82021.
XX
PT   New DNA sequences coding for protein C enzyme -
PT   and new expressed polypeptide(s), useful for detecting tumour
PT   promoting activity of test cpds.
XX
PS   Claim 1; Fig 1; 36pp; English.
XX
CC   PKC product can be used in determining tumour promoting properties
CC   of a test sample, and probes derived from the sequence may be used
CC   in isolating polypeptides from other species.
XX
SQ   Sequence 1802 BP; 490 A; 438 C; 476 G; 397 T; 1 other;
```

```
  Query Match            57.6%;  Score 19;  DB 9;  Length 1802;
  Best Local Similarity  100.0%;  Pred. No. 58;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 AAGAGTTTGTCAGTGGGAG 33
           |||||||||||||||||||
Db    1604 AAGAGTTTGTCAGTGGGAG 1586


RESULT 15
AAN90750/c
ID   AAN90750 standard; DNA; 2600 BP.
XX
AC   AAN90750;
XX
DT   11-JAN-1990  (first entry)
XX
DE   Protein kinase C beta 1 cDNA.
XX
KW   Protein kinase C beta 1; cellular growth control; tumorigenesis.
XX
OS   Rat.
XX
PN   WO8907654-A.
XX
PD   24-AUG-1989.
XX
PF   09-FEB-1989;   89WO-US00462.
XX
PR   10-FEB-1988;   88US-0154206.
XX
PA   (PROG ) PROGENICS PHARMACEUTICALS INC.
XX
PI   Housey GM;
XX
DR   WPI; 1989-263721/36.
DR   P-PSDB; AAP91373.
XX
PT   Screening for protein inhibitors and activators - by examining phenotypic
PT   changes of two cell lines having different protein prodn.
XX
PS   Disclosure; fig  1; 75pp; English.
XX
CC   Protein kinase C (PKC) beta 1 cDNA was sequenced from  clone RP58
CC   isolated from a rat brain cDNA library corresp. to clone RP41. PKC is a
CC   Ca2+ - and phospholipid dependent ser/thr protein kinase important in
CC   cellular growth control.
XX
SQ   Sequence 2600 BP; 676 A; 642 C; 670 G; 612 T; 0 other;

  Query Match            57.6%;  Score 19;  DB 10;  Length 2600;
  Best Local Similarity  100.0%;  Pred. No. 62;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      15 AAGAGTTTGTCAGTGGGAG 33
           |||||||||||||||||||
Db    2033 AAGAGTTTGTCAGTGGGAG 2015


Search completed: December 16, 2002, 11:13:01
Job time : 940 secs
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GenCore version 5.1.3

OM nucleic - nucleic search, using sw model

Run on: December 16, 2002, 10:54:59 ; Search time 3176 Seconds
(without alignments)
302.391 Million cell updates/sec

Title: US-09-435-471B-9
Perfect score: 33
Sequence: 1 gcattctagtcgacaagagtttgtcagtgggag 33

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	23.2	70.3	180673	10	AC068627	AC068627 Mus Muscu
c	2	22	66.7	11260	1	AE014010	AE014010 Yersinia
c	3	22	66.7	203728	1	AJ414160	AJ414160 Yersinia
c	4	21.8	66.1	113451	2	AC023297	AC023297 Homo sapi
c	5	21.8	66.1	200724	9	AL139382	AL139382 Human DNA
c	6	21.6	65.5	160708	2	AC011962	AC011962 Homo sapi
c	7	21.6	65.5	163823	9	AC097372	AC097372 Homo sapi
	8	21.4	64.8	199006	2	AC126835	AC126835 Rattus no
c	9	20.8	63.0	161308	2	AC122578	AC122578 Rattus no
	10	20.8	63.0	179250	2	AC128864	AC128864 Rattus no
	11	20.8	63.0	180035	2	AC117985	AC117985 Papio cyn
	12	20.8	63.0	180783	2	AC116932	AC116932 Papio cyn
c	13	20.8	63.0	183698	10	AL606464	AL606464 Mouse DNA
c	14	20.8	63.0	209876	2	AL627315	AL627315 Mus muscu
c	15	20.6	62.4	169514	2	AC122449	AC122449 Mus muscu
c	16	20.4	61.8	72781	2	AC018417	AC018417 Homo sapi
c	17	20.4	61.8	98240	9	AC006021	AC006021 Homo sapi
c	18	20.4	61.8	109244	2	AC109077	AC109077 Rattus no
	19	20.4	61.8	109395	2	AC013742	AC013742 Homo sapi
c	20	20.4	61.8	158987	9	AC108713	AC108713 Homo sapi
	21	20.4	61.8	180189	9	AL365510	AL365510 Human DNA
	22	20.4	61.8	184090	2	AC009564	AC009564 Homo sapi
c	23	20.4	61.8	198481	9	AC022389	AC022389 Homo sapi
c	24	20.2	61.2	40286	3	CEC05E7	Z67879 Caenorhabdi
c	25	20.2	61.2	124278	2	AC104618	AC104618 Homo sapi
	26	20.2	61.2	135706	2	AC102862	AC102862 Mus muscu
	27	20.2	61.2	161421	2	AC068114	AC068114 Homo sapi
	28	20.2	61.2	169226	9	AL590669	AL590669 Human DNA
c	29	20.2	61.2	179371	2	AC103130	AC103130 Rattus no
	30	20	60.6	892	3	AF302260	AF302260 Biomphala
	31	20	60.6	1496	1	UEU408960	AJ408960 Unculture
	32	20	60.6	24707	3	CEF14E5	Z66522 Caenorhabdi
	33	20	60.6	178893	2	AC120681	AC120681 Rattus no
	34	20	60.6	181911	2	AC098105	AC098105 Rattus no
	35	20	60.6	193006	2	AC120599	AC120599 Rattus no
c	36	19.8	60.0	401	6	AX270035	AX270035 Sequence
c	37	19.8	60.0	401	6	AX270036	AX270036 Sequence
c	38	19.8	60.0	401	6	AX271566	AX271566 Sequence
c	39	19.8	60.0	401	6	AX271567	AX271567 Sequence
c	40	19.8	60.0	2251	3	AY119516	AY119516 Drosophil
c	41	19.8	60.0	32814	8	SPAC22A12	Z99295 S.pombe chr
c	42	19.8	60.0	99895	2	AC114858	AC114858 Rattus no
c	43	19.8	60.0	106551	2	AC017423	AC017423 Drosophil
c	44	19.8	60.0	110000	9	AF491780_08	Continuation (9 of
c	45	19.8	60.0	137009	9	AC009970	AC009970 Homo sapi

ALIGNMENTS

RESULT 1
AC068627/c
LOCUS AC068627 180673 bp DNA linear ROD 15-MAY-2002
DEFINITION Mus Musculus Chromosome 5 RP23-389F6, complete sequence.
ACCESSION AC068627
VERSION AC068627.16 GI:13027370
KEYWORDS HTG.
SOURCE Mus musculus.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 180673)
AUTHORS Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
Gordon,M., Goltz,J.S. and Kucherlapati,R.

```
  TITLE     High Throughput Mouse Sequencing
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 180673)
  AUTHORS   Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
            Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
            Gordon,M., Goltz,J.S. and Kucherlapati,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-MAY-2000) Department of Molecular Genetics, Albert
            Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
            Bronx, NY 10461, USA
REFERENCE   3  (bases 1 to 180673)
  AUTHORS   Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
            Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
            Gordon,M., Goltz,J.S. and Kucherlapati,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2001) Department of Molecular Genetics, Albert
            Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
            Bronx, NY 10461, USA
REFERENCE   4  (bases 1 to 180673)
  AUTHORS   Grills,G., Han,J., Montgomery,K.T., Lee,E., Long,J., Pomerantz,R.,
            Ioshikhes,I.P., Shim,C., Decker,J., Thomas,E., Perera,A.,
            Gordon,M., Goltz,J.S. and Kucherlapati,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-2001) Department of Molecular Genetics, Albert
            Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
            Bronx, NY 10461, USA
COMMENT     On Feb 21, 2001 this sequence version replaced gi:11276096.
            ----------------Genome Center:
            Harvard Partners Genome Center
            Center Code:      HPGC
            Web site: http://www.hpcgg.org/Sequence/mouse.html
            Contact:  hpgc@mendel.mgh.harvard.edu

            CLONE LENGTH: This sequence represents the entire insert of this
            clone unless otherwise noted. If there are overlapping clones, the
            overlaps are noted in the beginning and end of the Features
            listing.

            ANNOTATION OF FEATURES:
               STSs are identified using ePCR (Genome Res. 7:541-550).
               Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
               Genes and Regions of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST
            and cDNA sequences in Unigene. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintain sequence continuity
            across the splice junctions. Sequences that are not identical
            matches are annotated as similar.

            SEQUENCING READ COVERAGE: Attempts are made to complete double
            stranded sequence for all regions.  All sequence is completed to a
            standard of coverage with a minimum of 3 reads with no ambiguities.
            If the sequence coverage for a region does not meet this standard,
            it is indicated in the annotation as Low Coverage.  Low coverage
            linkages are verified by PCR product size verification or
            verification of forward and reverse reads from clones which span
            the low coverage area.

            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
            standards - estimated average error rate is less than 1 per 10,000
            bases using the Consed quality parameters.  Regions that do not
            meet this requirement are annotated as Low Quality.

            ----------------Summary Statistics
            Center project name: ACQ
            Sequencing vector: pUC18; L08752
            Chemistry: Dye-terminator Big Dye; 100%
            Assembly program: Phrap version 0.990319
            Contig length: 180673
            Fraction of Phrap value < 40: 0.00121
            Error Rate in Consed: .01 per 10,000 bases
            Number of N's in consensus: 0
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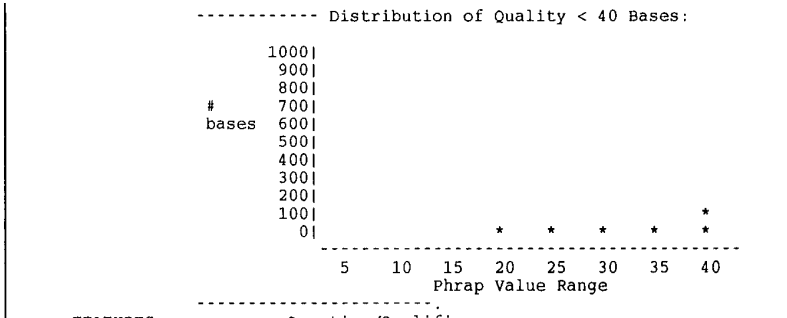


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                     /db_xref="taxon:10090"
                     /chromosome="5"
                     /clone="RP23-389F6"
     misc_feature    1. .45796
                     /note="Overlap with Clone RP23-327P24, AC084217"
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     repeat_region   complement(274. .410)
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     repeat_region   658. .694
                     /rpt_family="(TG)n"
     repeat_region   complement(695. .840)
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     repeat_region   1635. .1667
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     repeat_region   3396. .3424
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     repeat_region   3425. .3748
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                     /rpt_family="(CAAA)n"
     repeat_region   4113. .4161
                     /rpt_family="AT_rich"
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     repeat_region   5096. .5125
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     repeat_region   5932. .6099
                     /rpt_family="B3"
     repeat_region   6102. .6137
                     /rpt_family="(CA)n"
     repeat_region   6962. .7044
                     /rpt_family="B3"
     repeat_region   7119. .7151
                     /rpt_family="(CCCCCT)n"
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                     /standard_name="D5Mit286"
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     repeat_region   8466. .8555
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     repeat_region   11378. .11518
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  Query Match            70.3%;  Score 23.2;  DB 10;  Length 180673;
  Best Local Similarity  89.3%;  Pred. No. 6.7;
  Matches   25;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGT 28
          |||||||||||  |||||||||||| | |
Db 106672 GCATTCTAGTCCACAAGAGTTTGTTATT 106645


RESULT 2
AE014010/c
LOCUS       AE014010               11260 bp    DNA     linear   BCT 26-JUL-2002
DEFINITION  Yersinia pestis KIM section 410 of 415 of the complete genome.
ACCESSION   AE014010 AE009952
VERSION     AE014010.1  GI:21961093
KEYWORDS    .
SOURCE      Yersinia pestis KIM.
  ORGANISM  Yersinia pestis KIM
            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
            Yersinia.
REFERENCE   1  (bases 1 to 11260)
  AUTHORS   Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.,
            Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.,
            Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
            Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
            Blattner,F.R. and Perry,R.D.
  TITLE     Genome Sequence of Yersinia pestis KIM
  JOURNAL   J. Bacteriol. 184 (16), 4601-4611 (2002)
   PUBMED   12142430
REFERENCE   2  (bases 1 to 11260)
  AUTHORS   Deng,W., Burland,V., Plunkett,G. III, Boutin,A., Mayhew,G.F.,
            Liss,P., Perna,N.T., Rose,D.J., Mau,B., Zhou,S., Schwartz,D.C.,
            Fetherston,J.D., Lindler,L.E., Brubaker,R.R., Plana,G.V.,
            Straley,S.C., McDonough,K.A., Nilles,M.L., Matson,J.S.,
            Blattner,F.R. and Perry,R.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-FEB-2002) Genetics, University of Wisconsin, 445
            Henry Mall, Madison, WI 53706, USA
FEATURES             Location/Qualifiers
     source          1. .11260
                     /organism="Yersinia pestis KIM"
                     /strain="KIM"
                     /db_xref="taxon:187410"
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                     /gene="y4082"
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                     /gene="y4082"
                     /function="unknown"
                     /note="residues 24 to 110 of 110 are 32.95 pct identical
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                     (AL627266) hypothetical protein [Salmonella enterica
                     subsp. enterica serovar Typhi]"
                     /codon_start=1
                     /transl_table=11
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                     /db_xref="GI:21961094"
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                     DVINDYDF"
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                     /gene="y4083"
     CDS             990. .1466
                     /gene="y4083"
                     /function="unknown"
                     /note="residues 71 to 155 of 158 are 30.33 pct identical
                     to residues 102 to 190 of 195 from GenPept :
                     >emb|CAB53120.1| (AL109962) putative secreted protein
                     [Streptomyces coelicolor A3(2)]"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical"
                     /protein_id="AAM87626.1"
                     /db_xref="GI:21961095"
                     /translation="MTNRMKALMLVTHLAVFGAGTGLGIYILPILTAETNATAPEIQA
                     VKQSAKYTGEFSRNQKGSDAVHWAEGKLYVSEHEIAFEGEIAPGPDYKIYLTKTQADD
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     gene            complement(1635. .1991)
                     /gene="y4084"
     CDS             complement(1635. .1991)
                     /gene="y4084"
                     /note="residues 3 to 118 of 118 are 61.20 pct identical to
                     residues 5 to 120 of 120 from E. coli K12 : B3602;
                     residues 1 to 118 of 118 are 100.00 pct identical to
                     residues 1 to 118 of 118 from GenPept : >emb|CAC93519.1|
                     (AJ414160) conserved hypothetical protein [Yersinia
                     pestis]"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="AAM87627.1"
                     /db_xref="GI:21961096"
                     /translation="MKEHAEIKRLSDMLDALNHKDPTVIQQGNVELITQHMKEKEKLA
                     AEIQRLKEVRVKNLSAEAQKLAQLPFSRAITKKEQADMGTLKKAVRGIVVVHPMTALG
                     REMGLKEVTGYAKKAF"
     gene            complement(2240. .2794)
                     /gene="mtlR"
                     /note="y4085"
     CDS             complement(2240. .2794)
                     /gene="mtlR"
                     /function="regulator; degradation of small molecules;
                     Carbon compounds"
                     /note="residues 2 to 174 of 184 are 77.45 pct identical to
                     residues 22 to 191 of 195 from E. coli K12 : B3601;
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residues 1 to 181 of 184 are 75.69 pct identical to residues 21 to 198 of 198 from GenPept : >gb|AAD45387.1|AF166095_3 (AF166095) mtl operon repressor [Klebsiella pneumoniae]"
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/db_xref="GI:21961097"
/translation="MIEKKQAFENRVLEHLNAGKTVRSFLMAAVDLLAEALNILVVQI FRKDDYAVKYAVEPLLVGDGPLSELSVRLKLVYALGVITRHEYEDAELLMALREELNH DGTEYRFTDDEILGPFGELHCVDELPPVPTFLRPDEADASLIAMQRQRYQQMVRSTMV LSITELLSRISVKQVSKLSPLSQG"

gene complement(3001. .4269)
/gene="mtlD"
/note="y4086"

CDS complement(3001. .4269)
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/function="enzyme; degradation of small molecules; Carbon compounds"
/note="residues 36 to 417 of 422 are 75.65 pct identical to residues 1 to 382 of 382 from E. coli K12 : B3600"
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/protein_id="AAM87629.1"
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gene complement(4301. .6232)
/gene="mtlA"
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CDS complement(4301. .6232)
/gene="mtlA"
/function="transport; transport of small molecules; carbohydrates, organic acids, alcohols"
/note="residues 3 to 640 of 643 are 81.66 pct identical to residues 2 to 636 of 637 from E. coli K12 : B3599; residues 3 to 640 of 643 are 82.28 pct identical to residues 2 to 636 of 638 from GenPept : >gb|AAL22544.1| (AE008871) PTS family, mannitol-specific enzyme IIABC components [Salmonella typhimurium LT2]"
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/db_xref="GI:21961099"
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gene complement(6882. .7607)
/gene="y4088"

CDS complement(6882. .7607)
/gene="y4088"
/note="residues 14 to 226 of 241 are 53.05 pct identical to residues 49 to 261 of 276 from E. coli K12 : B3554; residues 14 to 226 of 241 are 52.11 pct identical to residues 9 to 221 of 236 from GenPept : >gb|AAL22507.1| (AE008869) putative outer membrane lipoprotein [Salmonella typhimurium LT2]"
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gene complement(8074. .10143)
/gene="glyS"
/note="y4089"

CDS complement(8074. .10143)
/gene="glyS"
/function="enzyme; aminoacyl tRNA synthetases, tRNA modification"
/note="residues 1 to 689 of 689 are 85.63 pct identical to residues 1 to 689 of 689 from E. coli K12 : B3559; residues 1 to 689 of 689 are 86.50 pct identical to residues 1 to 689 of 689 from GenPept : >gb|AAL22514.1| (AE008869) glycine tRNA synthetase, beta subunit [Salmonella typhimurium LT2]"
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Query Match 66.7%; Score 22; DB 1; Length 11260;
Best Local Similarity 83.3%; Pred. No. 29;
Matches 25; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCATTCTAGTCGACAAGAGTTTGTCAGTGG 30
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Db 8678 GCATTATCGTCGAAAAGAATTTGTCACTGG 8649

RESULT 3
AJ414160/c
LOCUS AJ414160 203728 bp DNA linear BCT 06-JUN-2002
DEFINITION Yersinia pestis strain CO92 complete genome; segment 20/20.
ACCESSION AJ414160 AL590842
VERSION AJ414160.1 GI:15981860
KEYWORDS .
SOURCE Yersinia pestis.
ORGANISM Yersinia pestis
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Yersinia.
REFERENCE 1 (bases 1 to 203728)
AUTHORS Parkhill,J., Wren,B.W., Thomson,N.R., Titball,R.W., Holden,M.T.G., Prentice,M.B., Sebaihia,M., James,K.D., Churcher,C., Mungall,K.L., Baker,S., Basham,D., Bentley,S.D., Brooks,K., Cerdeno-Tarraga,A.M., Chillingworth,T., Cronin,A., Davies,R.M., Davis,P., Dougan,G., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Leather,S., Karlyshev,A.V., Moule,S., Oyston,P.C.F., Quail,M., Rutherford,K., Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G.
TITLE Genome sequence of Yersinia pestis, the causative agent of plague
JOURNAL Nature 413 (6855), 523-527 (2001)
MEDLINE 21470413
PUBMED 11586360
REFERENCE 2 (bases 1 to 203728)
AUTHORS Parkhill,J.
TITLE Direct Submission
JOURNAL Submitted (04-OCT-2001) Submitted on behalf of the Yersinia sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk

```
COMMENT     Notes:
            Details of Y. pestis sequencing at the Sanger Centre are available
            on the World Wide Web.
            (URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
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                     /db_xref="taxon:632"
                     /note="biovar: Orientalis"
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                     /note="no significant database hits to the full length
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                     79 aa overlap)"
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                     scores: E(): 0, 59.1% id in 159 aa, and to Escherichia
                     coli thermoresistant gluconokinase GntK SW:GNTK_ECOLI
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                     transporter GntT SW:GNTT_ECOLI (P39835) (437 aa) fasta
                     scores: E(): 0, 84.5% id in 438 aa, and to Escherichia
                     coli Gnt-II system L-idonate transporter IdnT
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                     61.2% id in 438 aa"
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                     TAIATIFNADMGKTLLYGTLLAIPTVILAGPVYARFLKGIDKPVPEGLYNPKIFTDKE
                     MPSFGVSVSTALVPVILMALRAVAEMILPKGHSLLPYAEFFGDPVIATLIAVLIAIFT
                     FGLNRGRSVESVMETLSDSIKIIAMMLLVIGGGGAFKQVLVDSGIEQYIAGMMGNSGA
                     SPILMAWSIAALLRIALGSATVAAITAGGIVAPLIATTGASPELMVIAVGSGSVIFSH
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                     /note="PS00356 Bacterial regulatory proteins, lacI family
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                     /note="Similar to Escherichia coli hypothetical protein
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                     scores: E(): 0, 50.4% id in 234 aa"
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  Best Local Similarity   83.3%;  Pred. No. 23;
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Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGG 30
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Db  141825 GCATTATCGTCGAAAAGAATTTGTCACTGG 141796


RESULT 4
AC023297/c
LOCUS       AC023297               113451 bp    DNA     linear   HTG 03-MAR-2000
DEFINITION  Homo sapiens clone RP11-21H9, WORKING DRAFT SEQUENCE, 13 unordered
            pieces.
ACCESSION   AC023297
VERSION     AC023297.3  GI:7144965
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 113451)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens, clone RP11-21H9
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 113451)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
            Anderson,S., Baldwin,J., Barna,N., Beda,F., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
            Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P.,
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            Fenestor,J., Ferreira,P., FitzHugh,W., Forrest,C., Gage,D.,
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            Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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            Peterson,K., Pierre,N., Pisani,C., Pollara,V., Raymond,C.,
            Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S.,
            Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
            Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A.,
            Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B.,
            Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
            Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Mar 3, 2000 this sequence version replaced gi:7139552.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L4020
                Center clone name: 21_H_9
            -------------- Summary Statistics
                Sequencing vector: M13; M77815; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.960731
                Consensus quality: 106493 bases at least Q40
                Consensus quality: 109791 bases at least Q30
                Consensus quality: 111178 bases at least Q20
                Insert size: 138000; agarose-fp
                Insert size: 112251; sum-of-contigs
                Quality coverage: 3.5 in Q20 bases; agarose-fp
                Quality coverage: 4.3 in Q20 bases; sum-of-contigs
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            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 13 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     2264: contig of 2264 bp in length
            *     2265 2364: gap of      100 bp
            *     2365     6779: contig of 4415 bp in length
            *     6780 6879: gap of      100 bp
            *     6880    11332: contig of 4453 bp in length
            *    11333 11432: gap of      100 bp
            *    11433    17335: contig of 5903 bp in length
            *    17336 17435: gap of      100 bp
            *    17436    23308: contig of 5873 bp in length
            *    23309 23408: gap of      100 bp
            *    23409    28598: contig of 5190 bp in length
            *    28599 28698: gap of      100 bp
            *    28699    36183: contig of 7485 bp in length
            *    36184 36283: gap of      100 bp
            *    36284    44529: contig of 8246 bp in length
            *    44530 44629: gap of      100 bp
            *    44630    53672: contig of 9043 bp in length
            *    53673 53772: gap of      100 bp
            *    53773    62948: contig of 9176 bp in length
            *    62949 63048: gap of      100 bp
            *    63049    75673: contig of 12625 bp in length
            *    75674 75773: gap of      100 bp
            *    75774    92375: contig of 16602 bp in length
            *    92376 92475: gap of      100 bp
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                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .2264
                     /note="assembly_fragment"
     misc_feature    2365. .6779
                     /note="assembly_fragment"
     misc_feature    6880. .11332
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                    /note="assembly_fragment"
     misc_feature   11433. .17335
                    /note="assembly_fragment"
     misc_feature   17436. .23308
                    /note="assembly_fragment"
     misc_feature   23409. .28598
                    /note="assembly_fragment"
     misc_feature   28699. .36183
                    /note="assembly_fragment
                    clone_end:T7
                    vector_side:left"
     misc_feature   36284. .44529
                    /note="assembly_fragment"
     misc_feature   44630. .53672
                    /note="assembly_fragment"
     misc_feature   53773. .62948
                    /note="assembly_fragment
                    clone_end:SP6
                    vector_side:right"
     misc_feature   63049. .75673
                    /note="assembly_fragment"
     misc_feature   75774. .92375
                    /note="assembly_fragment"
     misc_feature   92476. .113451
                    /note="assembly_fragment"
BASE COUNT    34163 a  23042 c  23371 g  31675 t   1200 others
ORIGIN

  Query Match            66.1%;  Score 21.8;  DB 2;  Length 113451;
  Best Local Similarity  78.8%;  Pred. No. 30;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
          | ||||  || ||||||||||||  |  ||||||
Db  48392 GAATTCATGTTGACAAGAGTTTGGCTTTGGGAG 48360


RESULT 5
AL139382/c
LOCUS       AL139382              200724 bp    DNA     linear   PRI 30-NOV-2000
DEFINITION  Human DNA sequence from clone RP11-86N24 on chromosome 13, complete
            sequence.
ACCESSION   AL139382
VERSION     AL139382.12  GI:11493233
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 200724)
  AUTHORS   Blakey,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-2000) Sanger Centre, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
            requests: clonerequest@sanger.ac.uk
COMMENT     On Nov 30, 2000 this sequence version replaced gi:11322785.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence has been finished according to sequence map criteria
            as follows.  An attempt is made to resolve all sequencing problems,
            such as compressions and repeats, but not necessarily within known
            annotated repeat sequence elements.  Where the sequence is
            ambiguous, there is an annotation using the 'unsure' feature key.
            The following abbreviations are used to associate primary accession
            numbers given in the feature table with their source databases:
            Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
            on the WORMPEP database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
            was generated from part of bacterial clone contigs of human
            chromosome 13, constructed by the Sanger Centre Chromosome 13
            Mapping Group.  Further information can be found at
            http://www.sanger.ac.uk/HGP/Chr13
            RP11-86N24 is from the library RPCI-11.1 constructed at the Roswell
            Park Cancer Institute by the group of Pieter de Jong. For further
            details see http://bacpac.med.buffalo.edu/
            VECTOR: pBACe3.6
            This sequence is the entire insert of clone RP11-86N24 The true
            right end of clone RP11-117I13 is at 16379 in this sequence.
FEATURES             Location/Qualifiers
     source          1. .200724
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="13"
                     /clone="RP11-86N24"
                     /clone_lib="RPCI-11.1"
     misc_feature    49203
                     /note="Forced join. Assembly confirmed by restriction
                     digest"
BASE COUNT    60078 a  41888 c  40178 g  58580 t
ORIGIN

  Query Match            66.1%;  Score 21.8;  DB 9;  Length 200724;
  Best Local Similarity  78.8%;  Pred. No. 29;
  Matches   26;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
          | ||||  || ||||||||||||  |  ||||||
Db 108477 GAATTCATGTTGACAAGAGTTTGGCTTTGGGAG 108445


RESULT 6
AC011962/c
LOCUS       AC011962              160708 bp    DNA     linear   HTG 06-MAY-2001
DEFINITION  Homo sapiens chromosome 4 clone RP11-166K23 map 4, WORKING DRAFT
            SEQUENCE, 14 unordered pieces.
ACCESSION   AC011962
VERSION     AC011962.3  GI:8516050
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 160708)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Homo sapiens chromosome 4, clone RP11-166K23
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 160708)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
            Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
            Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
            Cooke,P., DeArellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
            Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
            Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
            Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
            Lehoczky,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N.,
            McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrim,J.,
            Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
            Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
            Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
            Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
            Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     On Jun 14, 2000 this sequence version replaced gi:7630664.
            All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
```

```
            Contact: sequence_submissions@genome.wi.mit.edu
           -------------- Project Information
            Center project name: L2589
            Center clone name: 166_K_23
           -------------- Summary Statistics
            Sequencing vector: M13; M77815; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.960731
            Consensus quality: 148088 bases at least Q40
            Consensus quality: 154421 bases at least Q30
            Consensus quality: 157062 bases at least Q20
            Insert size: 151000; agarose-fp
            Insert size: 159408; sum-of-contigs
            Quality coverage: 4.6 in Q20 bases; agarose-fp
            Quality coverage: 4.4 in Q20 bases; sum-of-contigs
           --------------.
           * NOTE: This is a 'working draft' sequence. It currently
           * consists of 14 contigs. The true order of the pieces
           * is not known and their order in this sequence record is
           * arbitrary. Gaps between the contigs are represented as
           * runs of N, but the exact sizes of the gaps are unknown.
           * This record will be updated with the finished sequence
           * as soon as it is available and the accession number will
           * be preserved.
           *       1     2140: contig of 2140 bp in length
           *    2141  2240: gap of     100 bp
           *    2241     5077: contig of 2837 bp in length
           *    5078  5177: gap of     100 bp
           *    5178    10215: contig of 5038 bp in length
           *   10216 10315: gap of     100 bp
           *   10316    14680: contig of 4365 bp in length
           *   14681 14780: gap of     100 bp
           *   14781    21149: contig of 6369 bp in length
           *   21150 21249: gap of     100 bp
           *   21250    26493: contig of 5244 bp in length
           *   26494 26593: gap of     100 bp
           *   26594    36585: contig of 9992 bp in length
           *   36586 36685: gap of     100 bp
           *   36686    43665: contig of 6980 bp in length
           *   43666 43765: gap of     100 bp
           *   43766    55870: contig of 12105 bp in length
           *   55871 55970: gap of     100 bp
           *   55971    66656: contig of 10686 bp in length
           *   66657 66756: gap of     100 bp
           *   66757    87066: contig of 20310 bp in length
           *   87067 87166: gap of     100 bp
           *   87167   109119: contig of 21953 bp in length
           *  109120 109219: gap of     100 bp
           *  109220   135181: contig of 25962 bp in length
           *  135182 135281: gap of     100 bp
           *  135282   160708: contig of 25427 bp in length.
FEATURES             Location/Qualifiers
     source          1. .160708
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4"
                     /clone="RP11-166K23"
                     /clone_lib="RPCI-11 Human Male BAC"
     misc_feature    1. .2140
                     /note="assembly_fragment"
     misc_feature    2241. .5077
                     /note="assembly_fragment"
     misc_feature    5178. .10215
                     /note="assembly_fragment"
     misc_feature    10316. .14680
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     misc_feature    14781. .21149
                     /note="assembly_fragment"
     misc_feature    21250. .26493
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     misc_feature    26594. .36585
                     /note="assembly_fragment"
     misc_feature    36686. .43665
                     /note="assembly_fragment"
     misc_feature    43766. .55870
                     /note="assembly_fragment"
     misc_feature    55971. .66656
                     /note="assembly_fragment"
     misc_feature    66757. .87066
                     /note="assembly_fragment"
     misc_feature    87167. .109119
                     /note="assembly_fragment"
     misc_feature    109220. .135181
                     /note="assembly_fragment"
     misc_feature    135282. .160708
                     /note="assembly_fragment"
BASE COUNT    48201 a  32652 c  31946 g  46605 t   1304 others
ORIGIN

  Query Match             65.5%;  Score 21.6;  DB 2;  Length 160708;
  Best Local Similarity   85.7%;  Pred. No. 36;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      4 TTCTAGTCGACAAGAGTTTGTCAGTGGG 31
          |||||||| ||| || |||||| |||||
Db 112934 TTCTAGTCCACATGATTTTGTCTGTGGG 112907


RESULT 7
AC097372/c
LOCUS       AC097372              163823 bp    DNA     linear   PRI 01-MAR-2002
DEFINITION  Homo sapiens BAC clone RP11-6L6 from 4, complete sequence.
ACCESSION   AC097372 AC010832
VERSION     AC097372.3  GI:16874901
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 163823)
  AUTHORS   Sulston,J.E. and Waterston,R.
  TITLE     Toward a complete human genome sequence
  JOURNAL   Genome Res. 8 (11), 1097-1108 (1998)
  MEDLINE   99063792
   PUBMED   9847074
REFERENCE   2  (bases 1 to 163823)
  AUTHORS   Cedroni,M., Kozlowicz,A. and Elliott,G.
  TITLE     The sequence of Homo sapiens BAC clone RP11-6L6
  JOURNAL   Unpublished (2001)
REFERENCE   3  (bases 1 to 163823)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-OCT-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   4  (bases 1 to 163823)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-NOV-2001) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   5  (bases 1 to 163823)
  AUTHORS   Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-JAN-2002) Genome Sequencing Center, Washington
            University School of Medicine, 4444 Forest Park Parkway, St. Louis,
            MO 63108, USA
REFERENCE   6  (bases 1 to 163823)
  AUTHORS   Waterston,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Department of Genetics, Washington
```

```
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT     On Nov 9, 2001 this sequence version replaced gi:16445193.
            -------------- Genome Center
                Center: Washington University Genome Sequencing Center
                Center code: WUGSC
                Web site: http://genome.wustl.edu/gsc
                Contact: sapiens@watson.wustl.edu
            -------------- Summary Statistics
                Center project name: H_NH0006L06
                Drafting Center: WIBR
            --------------.

            NOTICE:  This sequence may not represent the entire insert of this
            clone.  It may be shorter because we only sequence overlapping
            clone sections once, or longer because we provide a small overlap
            between neighboring data submissions.

            This sequence was finished as follows unless otherwise noted:
            all regions were double stranded, sequenced with an alternate
            chemistry, or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
            as compressions and repeats; all regions were covered by sequence
            from more than one subclone; and the assembly was confirmed by
            restriction digest.

            MAPPING INFORMATION:
            Mapping information for this clone was provided by Dr. John D.
            McPherson, Department of Genetics, Washington University, St. Louis
            MO. For additional information about the map position of this
            sequence, see http://genome.wustl.edu/gsc

            SOURCE INFORMATION:
            The RPCI-11 human BAC library was made from the blood of one male
            donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
            Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
            approach for construction of bacterial artificial chromosome
            libraries. Genomics 51:1-8. The clone may be obtained either from
            Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
            and coworkers at http://www.chori.org
            VECTOR:  pBACe3.6

            NEIGHBORING SEQUENCE INFORMATION:
            The clone sequenced to the left is RP11-203B7; the clone sequenced
            to the right is RP11-552I10, 2000 bp overlap.  Actual start of this
            clone is at base position 1 of RP11-6L6.

            Data from AC009875 was used to finish this clone, AC097372.

            The sequence of AC010832 has been incorporated into AC097372.
FEATURES                Location/Qualifiers
     source             1. .163823
                        /organism="Homo sapiens"
                        /db_xref="taxon:9606"
                        /chromosome="4"
                        /map="4"
                        /clone="RP11-6L6"
                        /clone_lib="RPCI-11"
     repeat_region      21. .50
                        /rpt_family="(TTTC)n"
     repeat_region      33. .160
                        /rpt_family="Alu"
     repeat_region      452. .759
                        /rpt_family="Alu"
     repeat_region      736. .758
                        /rpt_family="(TAAA)n"
     repeat_region      759. .793
                        /rpt_family="AT_rich"
     repeat_region      955. .1010
                        /rpt_family="MER1_type"
     misc_feature       2344. .2811
                        /note="match to EST AI791835 (NID:g5339477) nc46d05.y5"
     misc_feature       2344. .2762
                        /note="match to EST AI821600 (NID:g5440679) nc46d05.x5"
     misc_feature       2609. .2792
                        /note="match to EST AA228735 (NID:g1851396) nc46d05.r1"
     repeat_region      2825. .3467
                        /rpt_family="ERVL"
     repeat_region      4123. .4287
                        /rpt_family="MIR"
     repeat_region      6799. .6930
                        /rpt_family="MIR"
     repeat_region      7384. .7405
                        /rpt_family="AT_rich"
     repeat_region      7699. .8047
                        /rpt_family="MaLR"
     repeat_region      8343. .8703
                        /rpt_family="MER1_type"
     repeat_region      9536. .9595
                        /rpt_family="(TA)n"
     repeat_region      9609. .9629
                        /rpt_family="AT_rich"
     repeat_region      9614. .11418
                        /rpt_family="L1"
     repeat_region      11422. .11524
                        /rpt_family="L1"
     repeat_region      11525. .11710
                        /rpt_family="MER1_type"
     repeat_region      11711. .12027
                        /rpt_family="Alu"
     repeat_region      11832. .11852
                        /rpt_family="AT_rich"
     repeat_region      12011. .12035
                        /rpt_family="(TAAAA)n"
     repeat_region      12028. .12072
                        /rpt_family="MER1_type"
     repeat_region      12073. .12151
                        /rpt_family="L1"
     repeat_region      12191. .12354
                        /rpt_family="MER1_type"
     repeat_region      12276. .12321
                        /rpt_family="AT_rich"
     repeat_region      12370. .12731
                        /rpt_family="L1"
     repeat_region      13182. .13462
                        /rpt_family="Alu"
     repeat_region      13463. .13612
                        /rpt_family="ERV1"
     repeat_region      13464. .13583
                        /rpt_family="(GA)n"
     repeat_region      13685. .13877
                        /rpt_family="MIR"
     misc_feature       14321. .14348
                        /note="match to EST AI425053 (NID:g4270984) tg50g01.x1"
     repeat_region      14321. .14343
                        /rpt_family="(T)n"
     misc_feature       14321. .14341
                        /note="match to EST AI125330 (NID:g3593844) qd92e10.x1"
     repeat_region      15566. .15861
                        /rpt_family="Alu"
     repeat_region      16673. .16762
                        /rpt_family="MIR"
     repeat_region      17608. .17696
                        /rpt_family="MIR"
     repeat_region      18069. .18134
                        /rpt_family="MIR"
     repeat_region      18162. .18196
                        /rpt_family="MIR"
     misc_feature       18753. .19167
                        /note="match to EST AI125330 (NID:g3593844) qd92e10.x1"
     misc_feature       18799. .19167
                        /note="match to EST AI125266 (NID:g3593780) qd92a12.x1"
     repeat_region      18853. .18983
                        /rpt_family="CR1"
     repeat_region      19065. .19300
                        /rpt_family="MIR"
     repeat_region      19660. .19698
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                  /rpt_family="(CA)n"
     repeat_region   19971. .20054
                  /rpt_family="L2"
     repeat_region   20085. .20113
                  /rpt_family="(CAAAA)n"
     misc_feature    20123. .20294
                  /note="match to EST AA682233 (NID:g2669365) ah52b12.s1"
     repeat_region   20152. .20347
                  /rpt_family="MIR"
     misc_feature    20416. .20417
                  /note="match to EST AA781375 (NID:g2840706) aj25e07.s1"
     misc_feature    20460. .20774
                  /note="match to EST AA781375 (NID:g2840706) aj25e07.s1"

  Query Match           65.5%;  Score 21.6;  DB 9;  Length 163823;
  Best Local Similarity  85.7%;  Pred. No. 36;
  Matches   24;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       4 TTCTAGTCGACAAGAGTTTGTCAGTGGG 31
           |||||||| ||| || |||||| |||||
Db   65387 TTCTAGTCCACATGATTTTGTCTGTGGG 65360


RESULT 8
AC126835
LOCUS       AC126835               199006 bp    DNA     linear   HTG 10-JUL-2002
DEFINITION  Rattus norvegicus clone CH230-9B24, *** SEQUENCING IN PROGRESS ***,
            68 unordered pieces.
ACCESSION   AC126835
VERSION     AC126835.1  GI:21722693
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 199006)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J.,
            Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,
            Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E.,
            Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S.,
            Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C.,
            Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L.,
            Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H.,
            Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J.,
            Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E.,
            Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M.,
            Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,
            Moser,M., Neal,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N.,
            Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G.,
            Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L.,
            Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y.,
            Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G.,
            Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I.,
            Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H.,
            Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H.,
            Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S.,
            Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q.,
            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 199006)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     -------------- Genome Center
               Center: Baylor College of Medicine
               Center code: BCM
               Web site: http://www.hgsc.bcm.tmc.edu/
               Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
               Center project name: GDBV
               Center clone name: CH230-9B24
            -------------- Summary Statistics
               Sequencing vector: Plasmid;
               Chemistry: Dye-terminator Big Dye: 100% of reads
               Assembly program: Phrap; version 0.990329
               Consensus quality: 139089 bases at least Q40
               Consensus quality: 145464 bases at least Q30
               Consensus quality: 150336 bases at least Q20
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 68 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1403: contig of 1403 bp in length
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            *     1504     3061: contig of 1558 bp in length
            *     3062     3161: gap of unknown length
            *     3162     4558: contig of 1397 bp in length
            *     4559     4658: gap of unknown length
            *     4659     6132: contig of 1474 bp in length
            *     6133     6232: gap of unknown length
            *     6233     7712: contig of 1480 bp in length
            *     7713     7812: gap of unknown length
            *     7813     8880: contig of 1068 bp in length
            *     8881     8980: gap of unknown length
            *     8981    10301: contig of 1321 bp in length
            *    10302    10401: gap of unknown length
            *    10402    11411: contig of 1010 bp in length
            *    11412    11511: gap of unknown length
            *    11512    12948: contig of 1437 bp in length
            *    12949    13048: gap of unknown length
            *    13049    14182: contig of 1134 bp in length
            *    14183    14282: gap of unknown length
            *    14283    15460: contig of 1178 bp in length
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            *    15561    16805: contig of 1245 bp in length
            *    16806    16905: gap of unknown length
            *    16906    18428: contig of 1523 bp in length
            *    18429    18528: gap of unknown length
            *    18529    19864: contig of 1336 bp in length
            *    19865    19964: gap of unknown length
            *    19965    21006: contig of 1042 bp in length
            *    21007    21106: gap of unknown length
            *    21107    22206: contig of 1100 bp in length
            *    22207    22306: gap of unknown length
            *    22307    23657: contig of 1351 bp in length
            *    23658    23757: gap of unknown length
            *    23758    25200: contig of 1443 bp in length
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*    25201    25300: gap of unknown length
*    25301    26847: contig of 1547 bp in length
*    26848    26947: gap of unknown length
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*    28626    28725: gap of unknown length
*    28726    30230: contig of 1505 bp in length
*    30231    30330: gap of unknown length
*    30331    31442: contig of 1112 bp in length
*    31443    31542: gap of unknown length
*    31543    32563: contig of 1021 bp in length
*    32564    32663: gap of unknown length
*    32664    34731: contig of 2068 bp in length
*    34732    34831: gap of unknown length
*    34832    36545: contig of 1714 bp in length
*    36546    36645: gap of unknown length
*    36646    37805: contig of 1160 bp in length
*    37806    37905: gap of unknown length
*    37906    39636: contig of 1731 bp in length
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*    39737    41668: contig of 1932 bp in length
*    41669    41768: gap of unknown length
*    41769    43961: contig of 2193 bp in length
*    43962    44061: gap of unknown length
*    44062    46438: contig of 2377 bp in length
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*    56446    56545: gap of unknown length
*    56546    58770: contig of 2225 bp in length
*    58771    58870: gap of unknown length
*    58871    61480: contig of 2610 bp in length
*    61481    61580: gap of unknown length
*    61581    64286: contig of 2706 bp in length
*    64287    64386: gap of unknown length
*    64387    66987: contig of 2601 bp in length
*    66988    67087: gap of unknown length
*    67088    69099: contig of 2012 bp in length
*    69100    69199: gap of unknown length
*    69200    71985: contig of 2786 bp in length
*    71986    72085: gap of unknown length
*    72086    73999: contig of 1914 bp in length
*    74000    74099: gap of unknown length
*    74100    76895: contig of 2796 bp in length
*    76896    76995: gap of unknown length
*    76996    79677: contig of 2682 bp in length
*    79678    79777: gap of unknown length
*    79778    82188: contig of 2411 bp in length
*    82189    82288: gap of unknown length
*    82289    84497: contig of 2209 bp in length
*    84498    84597: gap of unknown length
*    84598    88360: contig of 3763 bp in length
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*    88461    92497: contig of 4037 bp in length
*    92498    92597: gap of unknown length
*    92598    96247: contig of 3650 bp in length
*    96248    96347: gap of unknown length
*    96348    99319: contig of 2972 bp in length
*    99320    99419: gap of unknown length
*    99420   102725: contig of 3306 bp in length
*   102726   102825: gap of unknown length
*   102826   106854: contig of 4029 bp in length
*   106855   106954: gap of unknown length
*   106955   110069: contig of 3115 bp in length
*   110070   110169: gap of unknown length
*   110170   112355: contig of 2186 bp in length
*   112356   112455: gap of unknown length
*   112456   115811: contig of 3356 bp in length
*   115812   115911: gap of unknown length
*   115912   120810: contig of 4899 bp in length
*   120811   120910: gap of unknown length
*   120911   126269: contig of 5359 bp in length
*   126270   126369: gap of unknown length

  Query Match             64.8%;  Score 21.4;  DB 2;  Length 199006;
  Best Local Similarity   80.6%;  Pred. No. 44;
  Matches   25;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           |||||| ||| ||| |||||| ||| | |||
Db   22157 CATTCTTGTCAACAGGAGTTTCTCACTCGGA 22187


RESULT 9
AC122578/c
LOCUS       AC122578              161308 bp    DNA     linear   HTG 12-JUL-2002
DEFINITION  Rattus norvegicus clone CH230-149L3, *** SEQUENCING IN PROGRESS
            ***, 76 unordered pieces.
ACCESSION   AC122578
VERSION     AC122578.2  GI:21728453
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 161308)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
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            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 161308)
```

```
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAY-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 161308)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Jul 11, 2002 this sequence version replaced gi:21205895.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: GHCC
                Center clone name: CH230-149L3
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 98694 bases at least Q40
                Consensus quality: 104469 bases at least Q30
                Consensus quality: 108317 bases at least Q20
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 76 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1324: contig of 1324 bp in length
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            *     1425     2840: contig of 1416 bp in length
            *     2841     2940: gap of unknown length
            *     2941     4430: contig of 1490 bp in length
            *     4431     4530: gap of unknown length
            *     4531     5562: contig of 1032 bp in length
            *     5563     5662: gap of unknown length
            *     5663     6677: contig of 1015 bp in length
            *     6678     6777: gap of unknown length
            *     6778     8046: contig of 1269 bp in length
            *     8047     8146: gap of unknown length
            *     8147     9215: contig of 1069 bp in length
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            *     9316    10537: contig of 1222 bp in length
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            *    10638    11753: contig of 1116 bp in length
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            *    14310    14409: gap of unknown length
            *    14410    15742: contig of 1333 bp in length
            *    15743    15842: gap of unknown length
            *    15843    17443: contig of 1601 bp in length
            *    17444    17543: gap of unknown length
            *    17544    18981: contig of 1438 bp in length
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            *    20559    22160: contig of 1602 bp in length
            *    22161    22260: gap of unknown length
            *    22261    23672: contig of 1412 bp in length
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            *    23773    25092: contig of 1320 bp in length
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            *    25193    26875: contig of 1683 bp in length
            *    26876    26975: gap of unknown length
            *    26976    28234: contig of 1259 bp in length
            *    28235    28334: gap of unknown length
            *    28335    29972: contig of 1638 bp in length
            *    29973    30072: gap of unknown length
            *    30073    31396: contig of 1324 bp in length
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            *    31497    33026: contig of 1530 bp in length
            *    33027    33126: gap of unknown length
            *    33127    34367: contig of 1241 bp in length
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            *    34468    36105: contig of 1638 bp in length
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            *    36206    38371: contig of 2166 bp in length
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            *    38472    40222: contig of 1751 bp in length
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            *    40323    41814: contig of 1492 bp in length
            *    41815    41914: gap of unknown length
            *    41915    43199: contig of 1285 bp in length
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            *    43300    45421: contig of 2122 bp in length
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            *    45522    47208: contig of 1687 bp in length
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            *    47309    48381: contig of 1073 bp in length
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            *    48482    49753: contig of 1272 bp in length
            *    49754    49853: gap of unknown length
            *    49854    51476: contig of 1623 bp in length
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            *    51577    54753: contig of 3177 bp in length
            *    54754    54853: gap of unknown length
            *    54854    56777: contig of 1924 bp in length
            *    56778    56877: gap of unknown length
            *    56878    58008: contig of 1131 bp in length
            *    58009    58108: gap of unknown length
            *    58109    60433: contig of 2325 bp in length
            *    60434    60533: gap of unknown length
            *    60534    62301: contig of 1768 bp in length
            *    62302    62401: gap of unknown length
            *    62402    64051: contig of 1650 bp in length
            *    64052    64151: gap of unknown length
            *    64152    65590: contig of 1439 bp in length
            *    65591    65690: gap of unknown length
            *    65691    66695: contig of 1005 bp in length
            *    66696    66795: gap of unknown length
            *    66796    68000: contig of 1205 bp in length
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            *    68101    69681: contig of 1581 bp in length
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            *    69782    71509: contig of 1728 bp in length
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            *    71610    72940: contig of 1331 bp in length
            *    72941    73040: gap of unknown length
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Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
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RESULT 10
AC128864
LOCUS       AC128864               179250 bp    DNA     linear   HTG 02-AUG-2002
DEFINITION  Rattus norvegicus clone CH230-422P24, *** SEQUENCING IN PROGRESS
            ***, 55 unordered pieces.
ACCESSION   AC128864
VERSION     AC128864.2  GI:22038232
KEYWORDS    HTG; HTGS_PHASE1.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 179250)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
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            Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S.,
            Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K.,
            Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
            Weinstock,G. and Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 179250)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 179250)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Aug 1, 2002 this sequence version replaced gi:21953007.
            -------------- Genome Center
                Center: Baylor College of Medicine
                Center code: BCM
                Web site: http://www.hgsc.bcm.tmc.edu/
                Contact: hgsc-help@bcm.tmc.edu
            -------------- Project Information
                Center project name: KAWO
                Center clone name: CH230-422P24
            -------------- Summary Statistics
                Sequencing vector: Plasmid;
                Chemistry: Dye-terminator Big Dye: 100% of reads
                Assembly program: Phrap; version 0.990329
                Consensus quality: 127967 bases at least Q40
                Consensus quality: 135422 bases at least Q30
                Consensus quality: 140879 bases at least Q20
            --------------
            * NOTE: Estimated insert size may differ from sequence length
            *   (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 55 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1     1509: contig of 1509 bp in length
            *     1510     1609: gap of unknown length
            *     1610     2783: contig of 1174 bp in length
            *     2784     2883: gap of unknown length
            *     2884     3895: contig of 1012 bp in length
            *     3896     3995: gap of unknown length
            *     3996     5157: contig of 1162 bp in length
            *     5158     5257: gap of unknown length
            *     5258     6448: contig of 1191 bp in length
            *     6449     6548: gap of unknown length
            *     6549     7719: contig of 1171 bp in length
            *     7720     7819: gap of unknown length
            *     7820     8882: contig of 1063 bp in length
            *     8883     8982: gap of unknown length
            *     8983    10855: contig of 1873 bp in length
            *    10856    10955: gap of unknown length
            *    10956    12045: contig of 1090 bp in length
            *    12046    12145: gap of unknown length
            *    12146    13327: contig of 1182 bp in length
            *    13328    13427: gap of unknown length
            *    13428    14604: contig of 1177 bp in length
            *    14605    14704: gap of unknown length
            *    14705    15815: contig of 1111 bp in length
            *    15816    15915: gap of unknown length
            *    15916    17158: contig of 1243 bp in length
            *    17159    17258: gap of unknown length
            *    17259    18348: contig of 1090 bp in length
            *    18349    18448: gap of unknown length
            *    18449    19561: contig of 1113 bp in length
            *    19562    19661: gap of unknown length
            *    19662    21326: contig of 1665 bp in length
            *    21327    21426: gap of unknown length
            *    21427    22575: contig of 1149 bp in length
            *    22576    22675: gap of unknown length
            *    22676    25291: contig of 2616 bp in length
            *    25292    25391: gap of unknown length
            *    25392    27995: contig of 2604 bp in length
            *    27996    28095: gap of unknown length
            *    28096    30167: contig of 2072 bp in length
            *    30168    30267: gap of unknown length
            *    30268    32001: contig of 1734 bp in length
            *    32002    32101: gap of unknown length
```

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          *    32102    34134: contig of 2033 bp in length
          *    34135    34234: gap of unknown length
          *    34235    36533: contig of 2299 bp in length
          *    36534    36633: gap of unknown length
          *    36634    38118: contig of 1485 bp in length
          *    38119    38218: gap of unknown length
          *    38219    40043: contig of 1825 bp in length
          *    40044    40143: gap of unknown length
          *    40144    42111: contig of 1968 bp in length
          *    42112    42211: gap of unknown length
          *    42212    44790: contig of 2579 bp in length
          *    44791    44890: gap of unknown length
          *    44891    46831: contig of 1941 bp in length
          *    46832    46931: gap of unknown length
          *    46932    49886: contig of 2955 bp in length
          *    49887    49986: gap of unknown length
          *    49987    53806: contig of 3820 bp in length
          *    53807    53906: gap of unknown length
          *    53907    56935: contig of 3029 bp in length
          *    56936    57035: gap of unknown length
          *    57036    59283: contig of 2248 bp in length
          *    59284    59383: gap of unknown length
          *    59384    61818: contig of 2435 bp in length
          *    61819    61918: gap of unknown length
          *    61919    65811: contig of 3893 bp in length
          *    65812    65911: gap of unknown length
          *    65912    68623: contig of 2712 bp in length
          *    68624    68723: gap of unknown length
          *    68724    71719: contig of 2996 bp in length
          *    71720    71819: gap of unknown length
          *    71820    76222: contig of 4403 bp in length
          *    76223    76322: gap of unknown length
          *    76323    80018: contig of 3696 bp in length
          *    80019    80118: gap of unknown length
          *    80119    83971: contig of 3853 bp in length
          *    83972    84071: gap of unknown length
          *    84072    87959: contig of 3888 bp in length
          *    87960    88059: gap of unknown length
          *    88060    91801: contig of 3742 bp in length
          *    91802    91901: gap of unknown length
          *    91902    97354: contig of 5453 bp in length
          *    97355    97454: gap of unknown length
          *    97455   100353: contig of 2899 bp in length
          *   100354   100453: gap of unknown length
          *   100454   105784: contig of 5331 bp in length
          *   105785   105884: gap of unknown length
          *   105885   110762: contig of 4878 bp in length
          *   110763   110862: gap of unknown length
          *   110863   114911: contig of 4049 bp in length
          *   114912   115011: gap of unknown length
          *   115012   120392: contig of 5381 bp in length
          *   120393   120492: gap of unknown length
          *   120493   126236: contig of 5744 bp in length
          *   126237   126336: gap of unknown length
          *   126337   132710: contig of 6374 bp in length
          *   132711   132810: gap of unknown length
          *   132811   139090: contig of 6280 bp in length
          *   139091   139190: gap of unknown length
          *   139191   143974: contig of 4784 bp in length
          *   143975   144074: gap of unknown length
          *   144075   148570: contig of 4496 bp in length
          *   148571   148670: gap of unknown length
          *   148671   153393: contig of 4723 bp in length
          *   153394   153493: gap of unknown length
          *   153494   159140: contig of 5647 bp in length

  Query Match             63.0%;  Score 20.8;  DB 2;  Length 179250;
  Best Local Similarity   78.1%;  Pred. No. 83;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
           || ||| ||| ||||| ||  || ||||||||
Db  129473 GCTTTCCAGTAGACAAAAGAATGGCAGTGGGA 129504
```

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RESULT 11
AC117985
LOCUS       AC117985               180035 bp    DNA     linear   HTG 12-APR-2002
DEFINITION  Papio cynocephalus anubis clone RP41-415A2, WORKING DRAFT SEQUENCE,
            5 unordered pieces.
ACCESSION   AC117985
VERSION     AC117985.1  GI:20143536
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Papio cynocephalus anubis.
  ORGANISM  Papio cynocephalus anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 180035)
  AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
            Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
            Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
            Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
            Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
            McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
            Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W.,
            Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 180035)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     ---------- Genome Center
                Center: NIH Intramural Sequencing Center
                Center code: NISC
                Web site: http://www.nisc.nih.gov
                Contact: nisc_zoo@nhgri.nih.gov
            ---------- Project Information
                Center project name: cqu
                Center clone name: 415A02
            ---------- Summary Statistics
                Sequencing vector: plasmid; n/a; 100% of reads
                Chemistry: Dye-terminator Big Dye; 100% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 178328 bases at least Q40
                Consensus quality: 178649 bases at least Q30
                Consensus quality: 178855 bases at least Q20
                Insert size: 182000; agarose-fp
                Insert size: 179635; sum-of-contigs
                Quality coverage: 9.97x in Q20 bases; agarose-fp
                Quality coverage: 10.10x in Q20 bases; sum-of-contigs
            ----------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 5 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *        1    21961: contig of 21961 bp in length
            *    21962    22061: gap of unknown length
            *    22062    41050: contig of 18989 bp in length
            *    41051    41150: gap of unknown length
            *    41151    72888: contig of 31738 bp in length
            *    72889    72988: gap of unknown length
            *    72989   119485: contig of 46497 bp in length
            *   119486   119585: gap of unknown length
            *   119586   180035: contig of 60450 bp in length.
FEATURES             Location/Qualifiers
     source          1. .180035
                     /organism="Papio cynocephalus anubis"
```

```
                     /db_xref="taxon:9555"
                     /clone="RP41-415A2"
                     /clone_lib="RP41"
     misc_feature    1. .21961
                     /note="assembly_fragment"
     misc_feature    22062. .41050
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
     misc_feature    41151. .72888
                     /note="assembly_fragment"
     misc_feature    72989. .119485
                     /note="assembly_fragment"
     misc_feature    119586. .180035
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:left"
BASE COUNT    53465 a  38533 c  37931 g  49705 t    401 others
ORIGIN

  Query Match            63.0%;  Score 20.8;  DB 2;  Length 180035;
  Best Local Similarity  78.1%;  Pred. No. 83;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           |||| |  |  | ||||||| |||||||||
Db   80872 CATTTTGTTACAGAAGAGTTTATCAGTGGGAG 80903


RESULT 12
AC116932
LOCUS       AC116932              180783 bp    DNA     linear   HTG 03-APR-2002
DEFINITION  Papio cynocephalus anubis clone RP41-156H4, WORKING DRAFT SEQUENCE,
            2 unordered pieces.
ACCESSION   AC116932
VERSION     AC116932.1  GI:19909406
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE      Papio cynocephalus anubis.
  ORGANISM  Papio cynocephalus anubis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
            Cercopithecinae; Papio.
REFERENCE   1  (bases 1 to 180783)
  AUTHORS   Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C.,
            Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J.,
            Haghighi,P., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E., Laric,P.,
            Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
            Margulies,E.H., Masiello,C., Maskeri,B., Mastrian,S.D.,
            McCloskey,J.C., McDowell,J., Paguirigan,C., Pearson,R.,
            Portnoy,M.E., Prasad,A., Schueler,M.G., Stantripop,S., Thomas,J.W.,
            Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
            Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.
  TITLE     NISC Comparative Sequencing Initiative
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 180783)
  AUTHORS   Green,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-APR-2002) NIH Intramural Sequencing Center, 8717
            Grovemont Circle, Gaithersburg, MD 20877, USA
COMMENT     -------------- Genome Center
                 Center: NIH Intramural Sequencing Center
                 Center code: NISC
                 Web site: http://www.nisc.nih.gov
                 Contact: nisc_mouse@nhgri.nih.gov
            -------------- Project Information
                 Center project name: cqt
                 Center clone name: 156H04
            -------------- Summary Statistics
                 Sequencing vector: plasmid; n/a; 100% of reads
                 Chemistry: Dye-terminator Big Dye; 100% of reads
                 Assembly program: Phrap; version 0.990319
                 Consensus quality: 180093 bases at least Q40
                 Consensus quality: 180363 bases at least Q30
                 Consensus quality: 180474 bases at least Q20
                 Insert size: 124000; agarose-fp
                 Insert size: 180683; sum-of-contigs
                 Quality coverage: 12.22x in Q20 bases; agarose-fp
                 Quality coverage: 8.38x in Q20 bases; sum-of-contigs
            --------------
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1    90657: contig of 90657 bp in length
            *   90658    90757: gap of unknown length
            *   90758   180783: contig of 90026 bp in length.
FEATURES             Location/Qualifiers
     source          1. .180783
                     /organism="Papio cynocephalus anubis"
                     /db_xref="taxon:9555"
                     /clone="RP41-156H4"
                     /clone_lib="RP41"
     misc_feature    1. .90657
                     /note="assembly_fragment
                     clone_end:SP6
                     vector_side:right"
     misc_feature    90758. .180783
                     /note="assembly_fragment
                     clone_end:T7
                     vector_side:right"
BASE COUNT    53019 a  40040 c  40244 g  47368 t    112 others
ORIGIN

  Query Match            63.0%;  Score 20.8;  DB 2;  Length 180783;
  Best Local Similarity  78.1%;  Pred. No. 83;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy       2 CATTCTAGTCGACAAGAGTTTGTCAGTGGGAG 33
           |||| |  |  | ||||||| |||||||||
Db   90608 CATTTTGTTACAGAAGAGTTTATCAGTGGGAG 90639


RESULT 13
AL606464/c
LOCUS       AL606464              183698 bp    DNA     linear   ROD 29-JUN-2002
DEFINITION  Mouse DNA sequence from clone RP23-462P2 on chromosome 13, complete
            sequence.
ACCESSION   AL606464
VERSION     AL606464.11  GI:16073721
KEYWORDS    HTG.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 183698)
  AUTHORS   Bates,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Oct 11, 2001 this sequence version replaced gi:16030239.
            During sequence assembly data is compared from overlapping clones.
            Where differences are found these are annotated as variations
            together with a note of the overlapping clone name. Note that the
            variation annotation may not be found in the sequence submission
            corresponding to the overlapping clone, as we submit sequences with
            only a small overlap as described above.
            This sequence was finished as follows unless otherwise noted: all
            regions were either double-stranded or sequenced with an alternate
            chemistry or covered by high quality data (i.e., phred quality >=
            30); an attempt was made to resolve all sequencing problems, such
```

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            as compressions and repeats; all regions were covered by at least
            one plasmid subclone or more than one M13 subclone; and the
            assembly was confirmed by restriction digest. The following
            abbreviations are used to associate primary accession numbers given
            in the feature table with their source databases: Em:, EMBL; Sw:,
            SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
            database can be found at
            http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-462P2 is
            from the RPCI-23 Mouse PAC Library
            constructed by the group of Pieter de Jong.
            For further details see http://www.chori.org/bacpac/home.htm
            VECTOR: pBACe3.6
            -------------- Genome Center
            Center: UK Medical Research Council
            Center code: UK-MRC
            Web site: http://mrcseq.har.mrc.ac.uk
            Contact: mouseq@har.mrc.ac.uk
            --------------.
FEATURES              Location/Qualifiers
     source           1. .183698
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /chromosome="13"
                      /clone="RP23-462P2"
                      /clone_lib="RPCI-23"
BASE COUNT    53761 a  39743 c  39566 g  50628 t
ORIGIN

  Query Match            63.0%;  Score 20.8;  DB 10;  Length 183698;
  Best Local Similarity   78.1%;  Pred. No. 83;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          ||||||||||| |||| ||||||| | ||
Db  66441 GCATTCTAGTCACCAAGCCTTTGTCAATAAGA 66410


RESULT 14
AL627315/c
LOCUS       AL627315              209876 bp    DNA     linear   HTG 19-JUN-2002
DEFINITION  Mus musculus chromosome 13 clone RP23-212D7, *** SEQUENCING IN
            PROGRESS ***, in ordered pieces.
ACCESSION   AL627315
VERSION     AL627315.7  GI:18135166
KEYWORDS    HTG; HTGS_PHASE2; HTGS_CANCELLED.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 209876)
  AUTHORS   Pearce,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-JUN-2002) Wellcome Trust Sanger Institute, Hinxton,
            Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
            humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
COMMENT     On Jan 11, 2002 this sequence version replaced gi:17048468.
            -------------- Genome Center
            Center: UK Medical Research Council
            Center code: UK-MRC
            Web site: http://mrcseq.har.mrc.ac.uk
            Contact: mouseq@har.mrc.ac.uk
            -------------- Project Information
            Center project name: bM212D7
            -------------- Summary Statistics
            Assembly program: XGAP4; version 4.5
            Sequencing vector: plasmid; L08752; 100% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Consensus quality: 209092 bases at least Q40
            Consensus quality: 209289 bases at least Q30
            Consensus quality: 209389 bases at least Q20
            Insert size: 209876; sum-of-contigs
            Insert size: 204253; 11.7% error; agarose-fp
            Quality coverage: 9.16x in Q20 bases; sum-of-contigs Quality
            coverage: 9.41x in Q20 bases; agarose-fp
            --------------.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES              Location/Qualifiers
     source           1. .209876
                      /organism="Mus musculus"
                      /db_xref="taxon:10090"
                      /chromosome="13"
                      /clone="RP23-212D7"
                      /clone_lib="RPCI-23"
     misc_feature     1. .209876
                      /note="assembly_fragment:04602"
BASE COUNT    60767 a  43745 c  44655 g  60709 t
ORIGIN

  Query Match            63.0%;  Score 20.8;  DB 2;  Length 209876;
  Best Local Similarity   78.1%;  Pred. No. 82;
  Matches   25;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy      1 GCATTCTAGTCGACAAGAGTTTGTCAGTGGGA 32
          ||||||||||| |||| ||||||| | ||
Db 190393 GCATTCTAGTCACCAAGCCTTTGTCAATAAGA 190362


RESULT 15
AC122449/c
LOCUS       AC122449              169514 bp    DNA     linear   HTG 05-JUL-2002
DEFINITION  Mus musculus chromosome UNK clone RP24-247O14, WORKING DRAFT
            SEQUENCE, 7 unordered pieces.
ACCESSION   AC122449
VERSION     AC122449.2  GI:21699710
KEYWORDS    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 169514)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     The sequence of Mus musculus clone
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 169514)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
REFERENCE   3  (bases 1 to 169514)
  AUTHORS   McPherson,J.D. and Waterston,R.H.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-JUL-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
COMMENT     On Jul 5, 2002 this sequence version replaced gi:21105910.

            ---------- Genome Center ----------
            Center: Washington University Genome Sequencing Center
            Center code: WUGSC
            Web site:http://genome.wustl.edu/gsc/index.shtml
            Contact: submissions@watson.wustl.edu
            ---------- Project Information ----------
            Center project name: M_BB0247O14
            ----------
            ---------- Summary Statistics ----------
            Sequencing vector: M13; 0%
            Sequencing vector: plasmid; 100%
            Chemistry: Dye-primer ET; 0% of reads
            Chemistry: Dye-terminator Big Dye; 100% of reads
            Assembly program: Phrap; version 0.990319
            Consensus quality: 166352 bases at least Q40
            Consensus quality: 166800 bases at least Q30
            Consensus quality: 167046 bases at least Q20
            Insert size: 169k; agarose-fp
```

```
            Insert size: 168914; sum-of-contigs
            Quality coverage: 0.00 in Q20 bases; agarose-fp
            Quality coverage: 11.90 in Q20 bases; sum-of-contigs
            ----------------------------------------------------.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 7 contigs. The true order of the pieces
            * is not known and their order in this sequence record is
            * arbitrary. Gaps between the contigs are represented as
            * runs of N, but the exact sizes of the gaps are unknown.
            * This record will be updated with the finished sequence
            * as soon as it is available and the accession number will
            * be preserved.
            *       1     1338: contig of 1338 bp in length
            *    1339     1438: gap of unknown length
            *    1439     6519: contig of 5081 bp in length
            *    6520     6619: gap of unknown length
            *    6620    17199: contig of 10580 bp in length
            *   17200    17299: gap of unknown length
            *   17300    26065: contig of 8766 bp in length
            *   26066    26165: gap of unknown length
            *   26166    82538: contig of 56373 bp in length
            *   82539    82638: gap of unknown length
            *   82639   168110: contig of 85472 bp in length
            *  168111   168210: gap of unknown length
            *  168211   169514: contig of 1304 bp in length.
FEATURES             Location/Qualifiers
     source          1. .169514
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
                     /chromosome="UNK"
                     /clone="RP24-247O14"
     misc_feature    1. .1338
                     /note="assembly_name:Contig13"
     misc_feature    1439. .6519
                     /note="assembly_name:Contig14"
     misc_feature    6620. .17199
                     /note="assembly_name:Contig15"
     misc_feature    17300. .26065
                     /note="assembly_name:Contig16"
     misc_feature    26166. .82538
                     /note="assembly_name:Contig17"
     misc_feature    82639. .168110
                     /note="assembly_name:Contig18"
     misc_feature    168211. .169514
                     /note="assembly_name:Contig9"
BASE COUNT    44433 a  39379 c  41318 g  43780 t    604 others
ORIGIN

  Query Match             62.4%;  Score 20.6;  DB 2;  Length 169514;
  Best Local Similarity   85.2%;  Pred. No. 1e+02;
  Matches   23;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 ATTCTAGTCGACAAGAGTTTGTCAGTG 29
           ||||||| | |||||| |||||||| |
Db   52765 ATTCTAGCCAACAAGAATTTGTCAGGG 52739


Search completed: December 16, 2002, 12:43:33
Job time : 3614 secs
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